Title: Perfect score: Sequence:

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protein search, using sw model

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

92612 seqs, 14418503 residues

Searched:

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published\_Applications\_AA: \*

Maximum

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length: 0 length: 2000000000

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Total number of hits satisfying chosen parameters:
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:/cgn2_6/ptodata/1/pubpaa/US07_EUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                  Sequence 34947, A
Sequence 36929, A
Sequence 2, Appli
Sequence 1360, Ap
Sequence 125, App
Sequence 125, App
Sequence 4, Appli
Sequence 716, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 1789, Ap
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PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 99/632, 366

PRIOR APPLICATION NUMBER: US 99/632, 366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 20/236, 359

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

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PRIOR APPLICATION NUMBER: PCT/US01/00665
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US-09-864-761-34947
; Sequence 34947, Application US/09864761
; Patent No. US20020048763A1
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36929, Application Patent No. US20020048763A1
                                                                                APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
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LENGTH: 188
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                                             PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27
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APPLICATION NUMBER: PCT FILING DATE: 2001-01-30
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ON: EXPRESSED IN HBLIOO, SIGNAL = 1.7

ON: EXPRESSED IN HBLART, SIGNAL = 0.92

ON: EXPRESSED IN HBART, SIGNAL = 0.92

ON: EXPRESSED IN HARROW, SIGNAL = 2.1

ON: EXPRESSED IN HARROW, SIGNAL = 1.8

ON: EXPRESSED IN HARIN, SIGNAL = 1.5

ON: EXPRESSED IN HARIN, SIGNAL = 1.5

ON: EXPRESSED IN HARIN, SIGNAL = 1.5

ON: EXPRESSED IN HARIN, SIGNAL = 0.95

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Pred. No. 1.4e-71;
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RESULT 3 US-09-850-799-2

Sequence 2, Application US/09850799 Patent No. US20020090647A1

GENERAL INFORMATION:
APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
APPLICANT: Hendricks, Timothy V.
APPLICANT: Hendricks, Timothy V.
APPLICANT: Description: Useful in the Treatment of N.
FILE REFERENCE: CASE-03828

Screening

of Compounds

CURRENT APPLICATION NUMBER: US/09/850,799

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Best Local
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OTHER INFORMATION: EXPRESSE
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36929
LENGTH: 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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               412 VTSSSFFAAPNPYWNSPTGGIYPN 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
OR APPLICATION NUMBER: US 09/608,408
OR FILING DATE: 2000-06-30
OR FILING DATE: 2001-01-29
DER OF SEQ ID NOS: 49117
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FILING DATE: 2001-01-30
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VTSSSFFAAPNPYWNSPTGGIYPN
                                                                              KVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALP
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                   N: EXPRESSED IN BT474, SIGNAL = 1.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1

N: EXPRESSED IN BRAIN, SIGNAL = 1.1

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.97

N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN HELIOO, SIGNAL = 1.4

N: EXPRESSED IN HELTO, SIGNAL = 1

N: EXPRESSED IN HELTO, SIGNAL = 1

N: SWISSPROT HIT: P11308, EVALUE 5.00e-87

N: EST_HUMAN HIT: BE831331.1, EVALUE 1.00e-59
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                                                                                                                                                                                                                                                                         32.5%;
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                                                                                                                                                                                                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                         Score 794;
Pred. No. 5.
144
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                       6e-59;
                                                                                                                                                                                                                                                                                            Length 144;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                   Gaps
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1360
                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
US-09-925-300-1360
                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-925-300-1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Rattus norvegicus US-09-850-799-2
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                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/360,779
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                           LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS 328
                                                                                                                                                  163 IDGKELCKMTKDDFQRLTPSYNADILLSHL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNATAAAAATAALYPTPGLQPPPGPFGAVAAASHLGGHY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPLSPAV-QKGSGQIQLWQFLLELLADRANAGCIAWEGGHGEFKLTDPDEVARRWGERKS 195
                                                 NTLGFGTEQAPYGMQTQNYPKGGLLDSMCPASTPSVLSSEQEFQMFPKSRLSSVSVTYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P------TGGIYPNTRLP-----AAHMPSHLGTYY 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAQDGALYKLPAGLAPLPFPGLS-----KLNLMAASAGVAPAGFS-----YWPG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPNMNYDKLSRALRYYYDKNIMSKVHGKRYAYRFDFQGLAQACQPPPAHAHAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340
                                                                                                                                                                                   l Similarity
89; Conserv
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                                                                                                                                                                                   Conservative
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28.8%;
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                                                                                                                                                                                 Score 344.5; DB 10;
Pred. No. 3.5e-21;
0; Mismatches 81;
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Pred. No. 1.2e-34;
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                                                                                IFPNTSVYPEATQRIT
                                                                                                                                                                                   Indels 109;
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                                                                                                                                                                                                                Length
                                                                                                                                                  -----HYLRE 197
                                                                                                                                                                                                                344;
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-125
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US-10-108-605-129
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                                                                                                                                                                                                         Sequence 129, Application US/10108605 Patent No. US20020160934A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 361
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 125
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                      APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Ramdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020160934A1
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
                                                                                                                          APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Broadus, Julie APPLICANT: Stam, Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AHQHPAAYMSTL------GLDK-GLLGGYTTQGGVPCFTGSGPIQLWQFLLE 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 SHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANP---GSGQIQLWQFLLE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
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                                                                                                                                                                                                                                                                                                                                                                                 KVHGKRYAYKF--DFHGIAQALQPHPPESSMYKY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGKRYAYKF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTAGKRYVYRFVCDL----QNLVGHTPEELVAKY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLDKTCQSFISWTGDGWEFKLTDPDEVARRWGIRKNKPKMNYEKLSRGLRYYYDKNIIH 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGKRYVYRF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSQDFPGSNLNLLTNNSGTPKDHDSPENGADSFESSDSLLQSWNSQSSLLDVQRVPSFES 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEDDCSQSLCLNKPTMSFKDYIQERSDPVEQGKPVIPAAVLAGFTGSGPIQLWQFLLELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 336; DB 9;
; Pred. No. 4.1e-20;
15; Mismatches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 623
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RESULT 7
US-09-866-356-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Sin
Matches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09866356 Patent No. US20020098543A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 129
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 SHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANP---GSGQIQLWQFLLE 291
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/866,356
FILING DATE: 29-May-2001
                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/055,113
FILING DATE: 1998-04-03
ATTORNEY/AGENT INFORMATION:
NRME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0501 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guegler, Karl J.

Lal, Preeti
TITLE OF INVENTION: PROSTATE-ASSOCIATED ETS PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                      SEQUENCE CHARACTERISTICS:
               IMMEDIATE SOURCE:
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                                                     TYPE: amino acid
STRANDEDNESS: single
LIBRARY: GenBank
                                        TOPOLOGY:
                                                                                                                                                                TELEX:
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                                                                                          LENGTH: 452 amino acids
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Corley, Neil C.
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                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 716, Application US/09925297 Patent No. US20020081659A1
                                                                                                                                Matches
                                                                                                                                               Query Match
Best Local Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/05989 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                          LENGTH: 203
TYPE: PRT
284 QLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRY 343
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                                                                                         230 RSAWTSHSHPTQSKATQP-----SSSTVPKTEDQRPQLDPYQIL-GPTSSRLANPGSGQI 283
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                                                      RGGYFSSSHEGFSYEKDPRLYFDDTCVVPERLEGKVKQEPTMYREGPPYQR-----RGSL 59
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Pred. No. 2.6e-19;
5; Mismatches 109;
                                                                                                                                                 Score 300.5; DB 1
Pred. No. 7.5e-18;
                                                                                                                                Mismatches
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US-09-126-945B-2
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                                                                                                                                                                                                  Sequence 1, Application US/09866356 Patent No. US20020098543A1 GENERAL INFORMATION:
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LENGTH: 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Prostate Derived Ets Factor FILE REFERENCE: 1488.1090000
CURRENT APPLICATION NUMBER: US/09/126,945B
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Libermann, Towia A.
APPLICANT: Oettgen, Joerg P.
APPLICANT: Kunsch, Charles A.
APPLICANT: Endress, Gregory A.
APPLICANT: Rosen, Craig A.
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ORGANISM: Homo sapiens
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                                                                                                                                   APPLICANT: Bandman, Olga
Corley, Neil C.
Guegler, Karl J.
                                                                                TITLE OF INVENTION: PROSTATE-ASSOCIATED NUMBER OF SEQUENCES: 4
                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   QVARLWGIRKNRPAMNYDKLSRSIRQYYKKGIIRKPDISQRLVYQF 331
                                                                                                                                                                                                                                                                                                                                                        EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKF 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRLPPMG-KAFQELAGKELCAMSEEQFRQRSP-LGGDVLHAHLDIWKSAAWMKERTSPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P---GGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPMDWSPSNVQKWLLWTEHQ
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Similarity 27.5%;
95; Conservative 4
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                    ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Dr.
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                                                                                                                       Preeti
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Pred. No. 4.8e-17;
0; Mismatches 106;
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                                                                                             Sequence 1789, Application Patent No. US20020136728A1 GENERAL INFORMATION:
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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    286 QVARLWGIRKNRPAMNYDKLSRSIRQYYKKGIIRKPDISQRLVYQF 331
                                                                                                                                                                                                                                                                         318 EVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 YGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLH------YLRER---GA
                                                                                                                                                                                                                                                                                                                                                    261 QLDPYQILGPTSSRLANPGSGQ-IQLWQFLLE-LLSDSSNSNCITW-EGTNGEFKMTDPD
                                                                                                                                                                                                                                                                                                                                                                                          224 IHYCASTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 P---GGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPMDWSPSNVQKWLLWTEHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GMNYGSYMEEKHI--PPPNMTTNE-----RRVIVPADPTLWSTDHVRQWLEWAVKE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 YPEDSSWAAKAPGASSREEPP-------EEPEQCPVIDSQAPAGSLDLV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 YGQTSKMSPRVPQQDWLSQPPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/866,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                               TFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRLPPMG-KAFQELAGKELCAMSEEQFRQRSP-LGGDVLHAHLDIWKSAAWMKERTSPGA
                                                                                                                                                                                                                                                                                                             -----TDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: PROSTUT12
CLONE: 1813005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/055,113 FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF-0501
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COMPOSITIONS AND METHODS FOR THE THERAPY
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27.5%;
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Pred. No. 4.8e-17;
                                                        Joy
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Indels 105; Length

Gaps

14;

165

200

223

317

235

335;

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SEQ ID NO 1789
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-528-1789
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US-10-033-528-1789
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Matches
                                                                                                                            Sequence 40154, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1789
LENGTH: 551
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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          APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
FILE REFERENCE: Acomica X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: King, APPLICANT: Meagh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                154 RPAMNYDKLSRSLRYYYEKGIMQKVAGERYVYKF 487
                                                                                                                                                                                                                                                                                                                  399
                                                                                                                                                                                                                                                                                                                                  269 GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 KPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKF 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 53; Conserv
                                                                                                                                                                                                                                                                                                                 GPPYQR-----RGALQLWQFLVALLDDPTNAHFIAWTGRGMEFKLIEPEEVARLWGIQKN 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meagher, Madeleine
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Pred. No. 7.8e-16;
4; Mismatches 22;
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Pred. No. 7.8
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22;
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                               BY MICROARRAY
                                             EXON NUCLEIC
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                                              FOR
                                         US-09-841-963A-2
US-09-841-963A-2
Sequence 2. Application US/09841963A
Patent No. US20020081601A1
GENERAL INFORMATION:
                                                                                                             RESULT 14
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                                                   Query Match
Best Local S
Matches 53
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PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2000-02-
PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2000-05-
PRIOR APPLICATION NUMBER: U
PRIOR PRIOR PRIOR DATE: 2000-08-
                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 40154 LENGTH: 55
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-9
NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: FILING DATE: 2001-01
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
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                                                  Similarity 96.4 53; Conservative
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                                                             11.48; 96.48;
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                                                  Score 279; DB 10;
Pred. No. 7.2e-17;
2; Mismatches 0;
                                                   0;
                                                   Gaps
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GENERAL INFORMATION:
APPLICANT: Watson, Dennis K.
APPLICANT: Papas, Takis S. (Deceased)
APPLICANT: Papas, Tula C. (Legal Representative)

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SEQ ID NO 1107

LENGTH: 304

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (258)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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US-09-764-864-1107
; Sequence 1107, Application US/09764864
; Patent No. US20020132753A1
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LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-963A-2
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.2%;
Best Local Similarity 26.6%;
Matches 92; Conservative 4
    Best Local Similarity 24.4 Matches 82; Conservative
                                               Query Match
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FILE REFERENCE: 10545-015-999
CURRENT APPLICATION NUMBER: US/09/841,963A
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION UNMBER: PCT/US99/27805
PRIOR APPLICATION NUMBER: PCT/US99/27805
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: PatentIn Ver. 2.0
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	Quer Best Matc	ESULT 1 S-08-878-177-2 Sequence 2, Application US/G Patent No. 6294354 GEMERAL INFORMATION: APPLICANT: Chugai Seiyaku R TITLE OF INVENTION: Cell Ce TITLE OF INVENTION: Cell Ce TITLE OF INVENTION: the Pro FILE REFERENCE: Chugai seiy CURRENT APPLICATION NUMBERS CURRENT FILING DATE: 1997-C NUMBER OF SEQ ID NOS: 7 SOFTWARE: PATENTIN VET. 2.0 SEQ ID NO 2 LENGTH: 451 TYPE: PRT ORGANIUSH: protein sequence S-08-878-177-2		22 22 22 22 22 23 24 24 24 24 24 24 24 24 24 24 24 24 24
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Sequence 4, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
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Patent No. 6294354
GENERAL INFORMATION:
APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, I
TITLE OF INVENTION: Cell Calcification Suppressing
TITLE OF INVENTION: the Proteins
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Best Local :
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CURRENT APPLICATION NUMBER: US/08/878,177
CURRENT FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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Best Local S
Matches 306
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APPLICANT:
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US-08-343-443B-4
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APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: ABDIT 1.0 DOS text ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FI
TITLE OF INVENTION: TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: AEDIT 1.0 DO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 230 South CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 -PVRVNYKREY--DHMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weiser, Gerard J
REGISTRATION NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/343,443B FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ 59
                                   LTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSH
                                                                                                                                                                                                                                                                                                TTNERRVIVPADPTLWTQEHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLR
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SGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSA
                                                                                                                                                    ATTLYNTEVLLSYLRE--SSLLAYNTTSHTDQSSRLSVKEDPSYDSVRRGAWGNNMN
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230 South Fifteenth St
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Pred. No. 9.5e
57; Mismatches
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RESULT 5
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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-360-779-2
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US-09-360-779-2
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TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases FILE REFERENCE: CASE-03828
CURRENT PELICATION NUMBER: US/09/360,779
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                              Sequence 2, Application US/09435335
Patent No. 6384204
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hondricks, Timothy J.
APPLICANT: Hondricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-04027
CURRENT APPLICATION NUMBER: US/09/435,335
CURRENT APPLICATION NUMBER: 09/360,779
EARLIER APPLICATION NUMBER: 09/360,779
EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                    428
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                                                                                                                                                                                                                                                                                                                                                                                                                P-----TGGIYPNTRLP-----AAHMPSHLGTYY 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAQDGALYKLPAGLAPLPFPGLS------KLNLMAASAGVAPAGFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PESSMYKYPSDL-----PYMSSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPNMNYDKLSRALRYYYDKNIMSKVHGKRYAYRFDFQGLAQACQPPPAHAHAAAAAAAAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPLSPAV-QKGSGQIQLWQFLLELLADRANAGCIAWEGGHGEFKLTDPDEVARRWGERKS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAAPNPYWNSPTGGIYPN---TRLPAAHMPSHLGTYY
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; Pred. No. 3.4e-40;
18; Mismatches 40
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; TYPE: PRT; ORGANISM: Rattus US-09-435-335-2
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Matches
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 110; Conserv
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APPLICANT: Sapru, Mohan K.
TITLE OF INVENTION: Neuregulin Response Element of the Reference: UMI-003
CURRENT APPLICATION NUMBER: US/09/092,636A
CURRENT FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                       94 QRRLGIPKNPWLWSEQQVCQWLLWATNEFSLVNVNLHQF-GMNGQMLCNLGKERFLELAP 152
FKMTDPDEVARRWGERKSKPMMYDKLSRALRYYYDKNIMTKVHGKRYAYKF
                                       YIQERSDPVEQGKP----VIPAAVLAGFTGSGPIQLWQFLLELLSDKSCQSFISWTGDGWE
                                                                                                                                                                                                                                SYNADILLSHL-----
                                                             TVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGE 310
                                                                                                                                                                           PNTSVY----PEAT-
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                                                                                            KDHDSPENGGDSFESSDSLLRSWNSQSSLLDVQRVPSFESFEEDCSQSLCLSKLTMSFKD
                                                                                                                                               PKDNLLDSMCPPSATPAALGSELQMLPKSRLNTVNVNYCSISQDFPSSNVNLLNNNSGKP
                                                                                                                                                                                                    DFVGDILWEHLEQMIKENQEKTEDQYEENSHLNAVPHWINSNTLGFSMEQAPYGMQAPNY 212
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ilarity 31.2%;
Conservative 3
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                                                                                                                     norvegicus
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                                                                                                                                                                                                                                                                                                          ; Score 424.5; DB 4;
; Pred. No. 4.3e-32;
34; Mismatches 93;
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                                                                                                                                                                                                                                                                                                                                   Length 468;
                                                                                                                                                                                                                                                                                                             Indels 115;
             362
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US-09-092-636-4
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                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08469412A Patent No. 5856125
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mavrot
APPLICANT: Blair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/092,636A
CURRENT FILING DATE: 198-06-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Neuregulin Response Element and Uses Therefor FILE REFERENCE: UMI-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sapru, Mohan K.
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TYPE: PRT
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                 APPLICANT: Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its
NUMBER OF SEQUENCES: 16
                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                            APPLICANT:
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                                                     COUNTRY:
                                                                       STATE:
                                                                                                       STREET:
                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   DGWEFKLADPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKTSGKRYVYRF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTMSFKDYIQERSDPVEQGKPVIPAAVLAGFTGSGPIQLWQFLLELLSDKSCQSFISWTG
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                                                                   San Francisco
California
                                                                                                       Two Embarcadero Center, Eighth Floor
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Blair, Donald G.
                                                                                                                                                                                                                                            Fisher, Robert J.
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                                                       USA
                                                                                                                                                                                                                          Beal Jr., Gregory J.
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                                                                                                                   Townsend and Townsend and Crew LLF
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Pred. No. 8.4e-32;
                                                                                                                                                                                                                                                                            George J.
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RESULT 9
US-09-021-715-7
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Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 SMYKYPSDLPYMSSYHAHPQKMNFVAP----HPPALPVTSSSFFAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 ANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYD 335
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 05-JUN-1995
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,715
                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Two Embarcadero Center, I
                                                                                                                                                                                                                                                                    Beal Jr., Gregory J.
Athanasiou, Meropi A.
Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLSRALRYYYNKRILHKTKGKRFTYKFNFNKLVLVNYPFIDMGLAGGAVPQSAPPVPSGG 131
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                                                                                                                                                                         STATE: California
                                                                                                                                                                                           CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                          Blair, Donald G.
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EM: PC-DOS/MS-DOS
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 NUMBER: US/09/021,715
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(first 8 amino acids from first exon no
included)"
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                                                                                                                                                                                                             Center, Eighth Floor
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                                       Version #1.30
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APPLICANT:
APPLICANT:
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                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                             SOFTWARE: Patentin Relaction CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          CITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 KLSRALRYYYDKNIMTKVHGKRYAYKFDFH------GIAQALQPHPPES 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYD 335
                                    APPLICATION NUMBER: US/08/469,412A FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                        STREET: Two Embarca
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHFRFPPSTP-----SEVLSPTEDPRSPPACSSSSSSLFSA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMYKYPSDLPYMSSYHAHPQKMNFVAP----HPPALPVTSSSFFAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLSRALRYYYNKRILHKTKGKRFTYKFNFNKLVLVNYPFIDMGLAGGAVPQSAPPVPSGG 131
                                                                                                                                                                                                                   94111-3834
                                                                                                                                                                                                                                                                                                                                                                      I: Sgouras, Dionyssios N. INVENTION: The ERF Genetic Locus and Its
Garrett-Wackowski, Eugenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "murine ERF au
(first 8 amino acids from first exon not
included)"
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                                                                                                                                                                                                                                                    California
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 543 amino acids
                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                     USA
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                                                                                                               PatentIn Release #1.0, Version #1.30
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1..543
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; MOLECULE TYPE: protein US-08-469-412A-2
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US-09-021-715-2
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Patent No. 6194547
GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             TELEPHONE: (415) 57
TELEFAX: (415) 57
INFORMATION FOR SEQ ID NO:
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mes 71; Conserv
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                                                                                                                                            REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,715
ETLING DATE: 10-Feb-1998
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sgouras, Dionyssios N. TITLE OF INVENTION: The ERF Genetic Locus and Its Products
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                          NAME: Garrett-Wackowski, EuREGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
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                                                                       ENGTH: 548 amino acids
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) 576-0300
MM: 2:
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42.5%; Pred. No. 5.8e-24;
tive 19; Mismatches 44
                                                                                                                              576-0300
SEQ ID NO:
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                                             Matches 106;
                                                                        Query Match
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                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/055,113 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  TELEPHONE: 650-855-0555
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: PROSTATE-ASSOCIATED ETS
NUMBER OF SEQUENCES: 4
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LIBRARY: Gen...
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Local Similarity
                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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Similarity 42.5%; Pred. No. 5.8
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                                             Conservative
                                                                                                                                     GenBank
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                                                                                                                                                                                single
                                                         13.3%; Score 324; DB 4; Length 452; 24.8%; Pred. No. 1.6e-22;
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                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILINGATION NUMBER: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gairett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Athanasiou, Meropi A APPLICANT: Sgouras, Dionyssios I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTY: San Francisco
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                    LENGTH:
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; SEQUENCE DESCRIPTION: US-09-021-715-11
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 Query Match
                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 YDKNIMTKVHGKRYAYKF 362
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGOUZAS, DIODYSSIOS N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  FEATURE:
                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mavrothalassitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                OTHER INFORMATION: /note= "ETS1 homologous region to ets-like ERF DNA-binding domain" ENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/021,715 FILING DATE: 10-Feb-1998 CLASSIFICATION: <Unknown>
                                                                                                           NAME/KEY: Domain LOCATION: 1..78
                                                                                                                                                                                                                                                                                                                                                                    NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                      LENGTH: 78 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fisher, Robert J
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 12.4%;
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Pred. No. 1.1e-21;
Score 303;
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Length
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78;
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Query Match
Best Local Similarity
""+"hes 57; Conserv
                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-343-443B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Peter, Martine
APPLICANT: Ploougastel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Tomas, Jeilles
TITLE OF INVENTION: UUCLEIC ACID CO
TITLE OF INVENTION: TRANSLATIONS AN
TITLE OF INVENTION: TRANSLATIONS AN
TITLE OF INVENTION: TRANSLACATIONS
TITLE OF INVENTION: TRANSLACATIONS
TITLE OF INVENTION: TRANSLACATIONS
NUMBER OF SEQUENCES: 129
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                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FR 9 FILING DATE: 20-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 18-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: AEDIT 1.0 DOS text editor
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230 South Fifteenth Street
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Desmaze, Chantal
                 Conservative
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## ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 1 AQ522081/c LOCUS COMMENT ACCESSION DEFINITION JOURNAL MEDLINE TITLE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,T.C., Smith,Y., Swartzell,S., Adams,M.D. a. Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong AQ522081 455 bp DNA linear GSS 11-MAY-HS\_5194\_Al\_D04\_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=770 Col=7 Row-G, DNA sequence.
AQ522081 99380589 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome  $% \left( 1\right) =\left\{ 1\right\}$ GSS AQ522081.1 GI:4769203 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) GSS 11-MAY-1999

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RESULT 2
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,

McCarter, M., Clifton, S., Kucaba, T., Theising, B., Bowers, Y.,

Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,

Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,

Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                (warwick.grant@agresearch.co.nz). The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis.
                                                                                                                                                                                                                                                                                                                    The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, N Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999 Unpublished (1999)
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kx01f12.yl Parastrongyloides trichosuri
Parastrongyloides trichosuri cDNA, mRNA
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                                                                                                                                                                                                                                                                      Nematodes provided by Dr. Warwick Grant of AgRearch, New Zealand
                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: McCarter JP
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Plate: 770 row: G column: 7
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                                                                                                                         primer: SL1 primer.
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and partially digested with a combination of EcoRI and
ECORI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
/organism="Parastrongyloides trichosuri"
/db_xref="taxon:131310"
/clone_lib="Parastrongyloides trichosuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="plate=770 Col=7 Row=G"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St.
Tel: 612 624 2755
Fax: 612 625 1738
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ESTs from r
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EST.
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Seg primer: SKmod (CTA gAA CTA g
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Texas A&M University:T262950e
TIGR sequence name:MTIAK87TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VandenBosch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kvandenb@cbs.umn.edu
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extracts. Plasmids containing com. ..... from the recombinant lambda-Zap phage using Ex-assist holor phage and propagated in XLOLR cells.
                                                  /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA. The cDNI was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                    /tissue_type="Seedling roots"
/dev_stage="24 hours post-inoumeliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pCRII-TOPO (Invitrogen) following the Topo TA cloning protocol. The cDNA insert can be excised by digestion with EcoRI. The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pCRII-TOPO; SL1-Oligo(dT) PCR-based library. Parastrongyloides trichosuri cDNA pcR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO (Invitrogen) following the Topo TA cloning
                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon_3880"
                                                                                                                                                                /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                    /clone_lib="KV1"
                                                                                                                                                                                                                                                                          /clone="pKV1-4P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV1 Medicago truncatula cDNA clone pKV1-4P5, mRNA
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/lab_host="DH10B"
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Contact: Long SR
Department of Biological Sciences and Howard Hughes Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
17; Conserv
 Pan troglodytes DNA, AG042409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanford University
Gilbert Biology, Stanford, CA 94305-5020,
Tel: 650 723 3232
Fax: 650 725 8309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: fa.srl@forsythe.stanford.edu
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                                                                                                                                                                                                                                 /tissue_type="Root hairs & tips"
/dev_stage="2-3 day old seedlings"
/note="Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
/note="Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
/note="Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
/note="Organ: Root; Vector: pBK-CMV and 2-3cm root tips
from elongating root hairs (30% w/w) and 2-3cm root tips
(70% w/w). XhoI-oligo-dT linker-primer and EcoRI
adaptors were used. cDNAs was cloned unidirectionally
into lambda ZAP Express (Stratagene), amplified, and
mass-excised into pBK-CMV vector plasmids. More
information is available at http://bio-SRL8.stanford.edu."
47 a 103 c 142 g 84 t 12 others
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/cultivar="Jemalong"
/db_xref="taxon:3880"
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              clone: PTB-020G15.F,
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              genomic survey sequence.
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       2 TCAGAGAGAGAGGAGCC 18
                                        Leishmania major Friedlin BAU unpublished (2002) other_GSSS: LB00701a.d_SP6.1 Contact: Myler PJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG042409.1 GI:16571134 GSS.
4 Nickerson Street,
Tel: 206 284-8846
                                                                                                    Ragland, M.
                                                                                                                                                                                                        Leishmania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes
                                                                                                                                                               Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Totoki,Y., Watanabe,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY
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R.Site 1 : SacI
R.Site 2 : SacI.
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100.0%;
            Seatttle,
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1 (bases 1 to 657)
Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sis, Aggarwal,G., Nelson,S., Seyler,A., Worthey,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                         LB00701a.d_T7.1 Leishmania major Friedlin BAC major genomic clone LB00701a, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                       Seattle Biomedical Research Institute
                                                                                                                                                                                                                                                                         Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC end sequences of Library PTB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-020G15.F.
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/clone_lib="PTB Chimpanzee Male BAC
/ 173 c 160 g 152 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-020G15.F"
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Pred. No.
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nd Sakaki, Y.
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WA 98109-1651, USA
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                                                                                                                                                                          Stuart, K. and
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                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999) Other_GSSs: CH230-19N18.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH230-19N18.TV CHORI-230 Segment 1
CH230-19N18, DNA sequence.
BH272744
                                                                                                                                                                                              Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                        (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 19 row: N column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., of Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Email: mylerpj@sbri.org
                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
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                                                                                                    primer: T7
ss: BAC ends.
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/lab_host="E. coli GeneHogs + TrfA"
/note="Vector: pCG270; Site_1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 Clones were
picked and arrayed in 384- and 96-will plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                            Location/Qualifiers
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/clone="LB00701a"
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/strain="Friedlin"
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TCAGAGAGAGAGGAGCC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM570 row: k column: 09
High quality sequence stop: 110.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
on Oct 3, 2000 this sequence version replaced gi:10573231.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_66"
/tissue_type="adenocarcinoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
240 c 254 g 262 t
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/Cell_type="Brain"
/Cell_type="Brain"
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/db_xref="taxon:9606"
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/clone_lib="CHORI-230 Segment 1"
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DKFZp686P0711_r1 686 (synonym: h
nkFZp686P0711 5', mRNA sequence.
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17; Conserv
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 380)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC66t2-RC6-NT0157-011100-011-E026t3=2000-11-016t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF919622 361 bp mRNA linear RC6-NT0157-011100-011-E02 NT0157 Homo sapiens cDNA, BF919622
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: nervous_tumor; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of the pucles o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue mRNA and cDNA amplification were low stringency conditions." 105 c 117 g 77 t
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source
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17; Conserv
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTCAGAGAGAGAGGAGCC
                                                                  Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE508198 385 bp mRNA linear EST 07-AUG-20 dc07b10.x1 NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3396379 similar to SW:CO3_XENLA P23667 COMPLEMENT C3 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other_ESTs: dc07b10.y1
High quality sequence stop: 1.
                        Trace considered overall poor quality 
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
1 (bases 1 to 385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE508198.1 GI:9727973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone (DKFZp686P0711) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Projec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No s1 sequence available.
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cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="human skeletal muscle"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="686 (synonym:
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Pred. No. 4.2e+03;
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MAGE:3396379 3'
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6, 1405
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BASE COUNT
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Dr. Judith F. Margolin
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM149896
458 bp mRNA linear TCAAP3Q10590 Pediatric acute myelogenous leukemia Baylor-HGSC project=TCAA Homo sapiens cDNA clone T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: M13 primer
/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; /note="Vector: lambda pSB; Site_1" BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored Xhol-oligo(dT) primer [5'GGAGGACTCGAGCGGCGCAGGAGGAG(T)VN 3'; V=A,C,G: N=A,C,G; T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTCGGATCCGCGCGCAATRAATRAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and Xhol and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/db_xref="taxon:8355"
/clone="IMAGE:3396379"
/clone_lib="NICHD XGC Lil"
/lab_host="DH1OB (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a xenopus Gene Collection (XGC)
) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
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/cell_type="myeloid cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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94.48;
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Pred. No. 4.2e+03;
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TCAAP1059, mRNA
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FEATURES

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COMMENT

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                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availa
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TgESTzz74f03.yl TgRH*-Tachyzoite cDNA Toxoplasma gondii cDNA clone TgESTzz74f03.yl 5', mRNA sequence.

AW702256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW702256.1 GI:7586409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW702256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sarcocystidae; Toxoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 319.
  Conservative
                                                                                                    /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was synthesized from poly mRNA using an
oligo-dT primer containing an XhoI site. Following second
strand synthesis, EcoRI adapters were ligated to the cDNA
and products were size-selected on sephacryl S500. The
cDNAs were ligated to EcoRI/ XhoI prepared lambda ZapII
(Stratagene). Clones were converted to phagemids by mass
excision using ExAssist helper phage and E.coli SOLR cells
(Stratagene). Insert sizes range from 0.3-3.0 kb. The
library may contain a small percentage of host or
bacterial contaminents. NOTE: Many clones lack the 5'
EcoRI site but contain the upstream polylinker sites."
69 a 166 c 112 g 131 t
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                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                         /strain="RH (Type I)"
/db_xref="taxon:5811"
/clone="TgESTZ74f03.y1"
/clone_1b="TgESTZ74f03.y1"
/clone_1b="TgESTZ74f03.y1"
/dev_stage="Tachyzoite"
/dev_stage="Tachyzoite"
/lab_host="SOLR cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
a 146 c 144 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Toxoplasma gondii"
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                     91.18;
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94.4%;
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                     Score 16.4; DB 10;
Pred. No. 4.7e+03;
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Pred. No. 4.
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.6e+03;
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  Indels
                                         Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                      449
                                                                                                                                                                                                                                         Local Similarity hes 17; Conserv
                                                                                                                                                  BQ331367 502 bp mRNA linear PM3-ET0272-300301-005-g12 ET0272 Homo sapiens cDNA, BQ331367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Bediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 490)
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Baylor-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: clones@txccc.org
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCGCAGGAGGAG(T)VN 3'; V-A,C,G; M-A,C,G,T] and then dC tailed. Second strand was primed with a BamH1-dC primer [5'AGAGAGCTCGGATCGCGGCGCAATAATAATAAT(C) 3'].

Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)*
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/clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="pediatric 6 years"
/lab_host="DH10B"
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/cell_type="myeloid cell"
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                                                                                                                                                                                                                                                             91.18;
94.48;
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                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                           Score 16.4; DB 13; Pred. No. 4.7e+03;
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                    mRNA sequence
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AUTHORS
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Search completed: November Job time: 42.1625 secs
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                                                                                     419 CTCAGAGGGAGAGGAGCC
                                                                                                                               1 CTCAGAGAGAGAGGAGCC 18
                                                                                                                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ331367.1 GI:20972466
EST.
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300301-005-g12&t3=2001-03-30&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases
                                                                                                                                                                                                                                                                                          118
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Location/Qualifiers
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                                                                                                                                                                                                                                                                               /note-"Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by choning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="ET0272"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.8e+03;
0; Mismatches 1
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1: /SIDS2/gcgdata/g

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SUMMARIES
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ABP41242	AAB54264	AAR44557	AAB85610	ABB59675	ABB62766	AAU75319	AAW07700	AAW07702	AAB56782	ABB66061	AAW78399	AAG74327	AAY90689	AAY98040	AAU75320	AAB87650	ABB62285	AAR33365	AA021529	AAU08495	AAG01336	ABB62865	ABB59502	AAM04949	AAM29754	AAM69423	AAM57033	ABB21631	ABB36259	ABB31070	ABG37017	AAM02964	AAM27682	AAM15221	
Human ovarian anti	Human pancreatic c	EWS/HUM-FLI-1 fusi	Mouse ETS suppress		phil	Erg t	ETS2		Human prostate can	Drosophila melanog	Rat Ets-2 protein.	colon	-+	Human ets2. Homo	Human ETS domain c	Bovine mammary tis	Drosophila melanog	Sequence of purine	Rat lambda73 prote	Rattus norvegicus	Human secreted pro	Drosophila melanog	Drosophila melanog	#3631	Peptide #3791 enco	Human bone marrow	rain ex	#3630	#3765		eptide		#1719	Peptide #1655 enco	

## ALIGNMENTS

RESULT 1
AAYO1520
ID AAYO
XX AAYO
XX Chic
XX C AAY01520 standard; Protein; 451 AA. Chicken C-11 protein. AAY01520; 23-JUN-1999 (first entry)

Chicken; C-11 protein; cell calcification inhibiting activity; cell calcification inhibiting agent; c-erg protein; arthritis deformans; ossification; spinal column ligament.

Gallus sp.

JP11075871-A.

23-MAR-1999

20-JUN-1997; 18-JUN-1997; 29-MAY-1998; 97US-0050297. 97US-0878177. 98JP-0166076

(CHUS ) CHUGAI PHARM CO LTD. (UYPE-) UNIV PENNSYLVANIA.

WPI; 1999-257708/22. N-PSDB; AAX26551.

An active protein for inhibiting cell calcification - useful for measuring the calcification of a cell, for diagnosing arthritis  $% \left( 1\right) =\left( 1\right) +\left( 1\right) +\left$ 

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RESULT 2
AAY01521
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Best Loc
Matches
                                                                                                                                        Chicken; C-11 protein; cell calcification inhibiting activity; cell calcification inhibiting agent; c-erg protein; arthritis ossification; spinal column ligament.
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RESULT 3
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XC AAU7
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AAU75313

AAU75313 standard;

protein;

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Human 23-APR-2002

Erg

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                     430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Page 9-10;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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    useful for arthritis

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The invention relates to an Erg (a member of the Ets family of C transcription factors) modulator for use in medicine, where the modulator cis is not tumour necrosis factor alpha (INF-alpha) or interleukin-1 (II-1). CA also included are a method of screening for a drug or drug candidate, cinvolving determining whether or not a group being screened modulates can be used in volving determining whether or not a group being screened modulates. CC involving determining whether or not a group being screened modulates. CC considering member), intracellular adhesion molecule-2 (ICAM-2) and/or von Willebrand Factor (VWF) RNA or polypeptide expression, or convolving the control of one or more regulatory sequences of the SPAC, CC TSP, rho A, ICAM-2 and/or vWF genes, determining whether or not a group being screened modulates the expression of Erg or of Erg RNA in a given convolving screened modulates the expression of Erg or not a group being screened modulates the expression of Erg or of Erg RNA in a given convolved, including of Erg to a nucleic acid comprising an Erg binding site, determining whether or not a nucleic acid hybridises with DNA of an Erg gene or its transcription product or determining whether or not a group being screened in the diagnosis of a disorder such as a disorder in colleic acid knocks out or reduces expression of Erg. Erg based to probes can be used in the diagnosis of a disorder such as a disorder in colleic acid knocks out or reduces expression of Erg. Erg based to a storder that can be treated by tissue remodeling, cancer, cancer compression, on the collect acid sorder, developmental collect acid sorder, in the preparation of a medicament for treating a collect agent is useful in the preparation of space, TSP, rho A, ICAM-2 or vWF. A group that modulates the effect of Erg or a therapeutically active agent is useful for the preparation of a medicament for treating calcius acid sequence of human Erg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Erg; transcription factor; tumour necrosis factor-alpha; TNF-alpha; interleukin-1 (IL-1); SPARC; thrombospondin; TSP; rho-A; intracellular adhesion molecule-2; ICAM-2; von Willebrand Factor; vangiogenesis; inflammatory disorder; developmental disorder; wound; menstrual disorder; cancer; rheumatoid arthritis; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy; restenosis; osteoporosis; cataract; diabetes mellitus; glomerulonephritis; inflammatory glomerular disease; vasculitis; retinopathy; liver fibrosis; haemoglobinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 53-54; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating cancer, rheumatoid arthritis, atherosclerosis, restenosis, and osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modulator of a member of the Ets family of transcription factors, Erg, which is not tumour necrosis factor alpha or interleukin-1, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLaughlin
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                                                                                               Erg.
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Local

Similarity

89.3%;

Score 2182; DB 23; Pred. No. 5.4e-188; Mismatches

Length

462; 14;

Gaps

4.

Disclosure;

Fig

7;

123pp; French

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RESULT 4
AAR44556
ID AAR4
XX AAR4
AC AAR4
XX AAR4
XX Ews
Chrc
KW Ews
KW Ews
KW huma
XX HOMC
COS HOMC
XX WO92
XX 19-1
XX 25-1
XX 20-1
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                                                                                                                                                                                                                                                                   chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene; malignant melanoma; hum-fil-1; clone BM025; primitive peripheral neuroectodermal tumour; human chromosome human chromosome 22; ss.
                                                                                                            Aurias A,
Plougastel
                                                New nucleic acid of EWS gene and its hybrid(s) sequence involved in chromosomal trans-location
                                                                                N-PSDB;
                                                                                                                                                              20-MAY-1992;
                                                                                                                                                                                  19-MAY-1993;
                                                                                                                                                                                                       25-NOV-1993.
                                                                                                                                                                                                                           W09323549-A
                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                          26-MAY-1994
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                                                                                                                                           (CNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGHGHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNADILLSHLHYLRETPLPHL---TS--DDVDKALQNSPRLMHARNTDLPYEPPRRSAW
                                      probes, fusion
                                                                                                                                          ) CNRS
                                                                               AAQ50644.
                                                                                                            Delattre O, B, Thomas
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                                                                                                                                          CENT NAT
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                                                                                                                                                              92FR-0006123
                              and
                              proteins etc., melanoma
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                                                                                                                                          RECH
                                                                                                            Desmaze C,
Zucman J;
                                                                                                                                          SCI.
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                                                                                                                      Melot
                                      diagnosis and
                                                  location,
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RESULT 5
AAB90792
ID AAB9
XX AAB9
XX AAB9
AC AAB9
XX Huma
XX Huma
XX Huma
XX Homo
XX NO1-C
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Best Local S
Matches 306
                       Nojima
Kuga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The probe 11RR1 was used to screen a human marrow cDNA library (Clontech cat.# Hr1058). The clone BM025 was identified and sequenced. It represents the entire coding region together with 5'- and 3'-UTRS of the Hum:Fli-1 gene.
                                                                                        (KYOW)
                                                                                                                                                                                                                                                                                                                                                                                    arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human shear stress-response protein
                                                                                                                                                           01-OCT-1999;
                                                                                                                                                                                                    02-OCT-2000;
                                                                                                                                                                                                                                                   12-APR-2001
                                                                                                                                                                                                                                                                                            WO200125427-A1
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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    ан, т. Sekine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PVRVNVKREY--DHMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
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                                                                                        KYOWA HAKKO KOGYO
NOJIMA H.
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                    Yoshisue H, Obayı
ekine S, Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 AA;
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ilarity 67.0%;
Conservative 5
                                                                                                                                                                                                    2000WO-JP06840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                      99JP-0280976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                       Obayashi
amura Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
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Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                       protein; vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
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                    M, Ota
Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:
                                         Ota
             S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
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                                            Kawabata
                                            2
                                            Sakurada
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RESULT 6
ABB29050
ID ABB2
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AC ABB2
XX
AC ABB2
XX
AC ABB2
XX
DE Pept
XX
DE Pept
XX
DE Pept
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DE Home
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Home
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PD WO20
PN 09-A
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Best Local Simi
Matches 304;
                                                                                                                                                                                  ABB29050 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                  WO200157271-A2
                                                                               disease;
                                                                                       Human; microarray;
                                                                                                             Peptide #1701 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                      01-FEB-2002
                                                                                                                                                            ABB29050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 60; Page 467-469; 678pp; Japanese.
                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences, proteins useful in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-266308/27.
N-PSDB; AAH02915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSH
                                                                                                                                                                                                                                                              FAAPNPYWNSPTGGIYPN---TRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                  YAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSQHAHQQKVNFVPPHPSSMPVTSSSF
                                                                                                                                                                                                                                                                                                                                           NSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                                                       ATTLYNTEVLLSHLSYLRE--SSLLAYNTTSHTDQSSRLSVKEDPSYDSYRRGAWGNNMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TINERRVIVPADPTLWTQEHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
                                                                                                                                                                                                                                                                                                                              NASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                                            SGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSA
                                                                             cancer
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                                                                                                                                     (first entry)
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                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by them and antibodies against them treatment of vascular disease caused by
                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1599; DB 22;
Pred. No. 2.2e-135;
                                                                                        probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                  ₽
                                                                                        gene expression; breast;
                                                                                                                                                                                                                                                              451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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30-JAN-2001;

2001WO-US00662

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RESULT 7
ABB34212
ID ABB3
XX
AC ABB3
XX
DT 04-F
XX
DE Pept
XX
KW Huma
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Best Local
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for etermining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                    Peptide #1718 encoded by human foetal liver single exon probe
                                                                 04-FEB-2002
                                                                                          ABB34212;
                                                                                                                     ABB34212 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                        132
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                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spatially-addressable set of single ful for measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                     AHPQKMNEVAPHPPALPVTSSSEFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the ed specification, but was obtained in electronic format dir WIPO at ftp.wipo.int/pub/published_pct_sequences.
             foetal liver;
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises number of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                   Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to a spatially-addressable set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO 12018; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                       ΑĄ,
           gene expression;
                                                                                                                                                                                                                                                                                                                                                              38.8%;
95.5%;
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                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                  Score 948; DB
Pred. No. 3.2e
4; Mismatches
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                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ingle exon nucleic acid probes, on in sample derived from humar exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR
           single
                                                                                                                                                                                                                                                                                                                                                              DB 22;
.2e-77;
            exon
                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                           Length 188;
           nucleic acid
                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
           probe
                                                                                                                                                                                                                                                                                                                                               Gaps
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片 Ş 밁 δÃ 밁 Q

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RESULT 8
ABB19649
ID ABB1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
Homo sapiens
                                                         Human; gene
cardiovascu
                                                                                                               Protein #1648 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 26847; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
                                       congenital heart disease
                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                            ABB19649;
                                                                                                                                                                                                                                ABB19649 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SG,
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                                                                                                                                                                                                                                                                                                                                                                                                     DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYH
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                                                         gene expression; heart; microarray; vascular systo
vascular disease; hypertension; cardiac arrhythmia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                     (first entry)
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2000US-0236359.
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                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.8%;
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                                                       hypertension;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon nucleic acid probes useful for n human fetal liver -
                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 948; DB 22
Pred. No. 3.2e-77
                                                                                                               for measuring heart cell gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank
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RESULT 9
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ID AAM5
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Best Local 9
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
 WO200157275-A2
                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizoph epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system expression are disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single
hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                      Human brain
                                                                                                                              05-NOV-2001
                                                                                                                                                         AAM55005;
                                                                                                                                                                                 AAM55005 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                          sapiens
                                                                                                                                                                                                                                             DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                                                                                                                                                                                                                                                  LANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG
                                                                                                                                                                                                                                                                                                 DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYH
                                                                                                                                                                                                                                                                                                                                                   LTSLGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 AA;
                                                                                                     expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to single exon
                                                                                                                             (first
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                                                                                                                                                                                 Protein;
                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                     Score 948; DB 22;
Pred. No. 3.2e-77;
4; Mismatches 4;
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                                                                                                                                                                                 B
                                                                                                   probe encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                             schizophrenia
                                                                                                     SEQ
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Best Local (
                                                                                                                                                                                                                                                                                                       Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                WO200157276-A2
                                                                                 microarray;
                                                                                         Human; bone
                                                                                                        Human bone marrow expressed probe encoded protein
                                                                                                                           06-NOV-2001
                                                                                                                                            AAM67391;
                                                                                                                                                          AAM67391 standard;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                      132
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                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                             DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                                                                                                                    SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                                                                                                                                                                                       188
                                                                                marrow expressed exon;
cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
2000US-0236359.
                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                       Ā,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DK,
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                                                                                                                                                          Protein;
                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                              38.8%;
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                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                              Score
Pred.
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                                                                                 lymphoma;
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                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                              948; DB 22;
No. 3.2e-77;
                                                                                         gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                 myeloma
                                                                                                                                                                                                                                                                                                       ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                         Listing;
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                                                                                                         SEQ
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04-FEB-2000;

2000US-0180312

30-JAN-2001; 2001WO-US00668

09-AUG-2001

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Best Local S
Matches 169
       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                               09-AUG-2001.
                                                                                                                                  Homo
                                                                             30-JAN-2001;
                                                                                                               WO200157278-A2
                                                                                                                                                  cervical cancer
                                                                                                                                                                           Peptide #1655 encoded
                                                                                                                                                                                             12-OCT-2001
                                                                                                                                                                                                              AAM15221;
                                                                                                                                                                                                                               AAM15221 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                       DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single
zing gene expression in
                                                                                                                                                        human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
; 2000US-0236359.
                2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                            2000US-0180312.
                                                                             2001WO-US00670
                                                                                                                                                                                            (first
         2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                        Score 948; DB 22; Pred. No. 3.2e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                          measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow
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RESULT 12
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Best Local
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                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                          09-AUG-2001.
                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                           Peptide #1719
                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                     AAM27682;
                                                                                                                                                                                                                                                                                                          AAM27682 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                     30-JAN-2001;
                                                                                                                                                                                      Homo
                                                                                                                                                                                                           genetic
                                                                                                                                                                                                                       Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical cancer
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          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                             AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                      DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH
                                                                                                                                                                                                                                                                                                                                                                 AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSHLGTYY
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                                                                                                                                                                                                                     microarray;
          MOLECULAR
                                                                                                                                                                                                           disorder.
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                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                     2001WO-US00663
                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                           encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID No 20047;
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           DYNAMICS
                                                                                                                                                                                                                     human;
                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                              entry;
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                                                                                                                                                                                                                                          by probe
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                                                                                                                                                                                                                     placenta;
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                                                                                                                                                                                                                                                                                                          188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic acid probes useful for human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 948; DB Pred. No. 3.2e 4; Mismatches
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                                                                                                                                                                                                                                         for measuring placental gene
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                                                                                                                                                                                                                     antenatal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
.2e-77;
                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 188;
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                                                                                                                                                                                                                                          expression.
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                                                                                                                                                                                                                                                                                                                                                                 188
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RESULT 13
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ID AAM02
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Best Local Sim
Matches 169;
                                                                                                                                            04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                         WPI;
                                                                                                                                                                                                                                                   WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
           Novel single exon nucleic acid
in a human breast -
                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                     29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; developinflammatory disease; proliferative breast disease;
                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                       09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 AAM02964 standard;
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                                                                SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 334
         human
                                          2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTSLGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSHLGTYY 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorders.
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                                                                                      MOLECULAR DYNAMICS
                                                                Hanzel
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         breast
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                                                                                                           2000US-0180312
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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95.5%;
                                                               Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon nucleic acid probes useful
n human placenta –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 948; DB 22;
Pred. No. 3.2e-77;
                   probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                Rank
                                                                                                                                                                                                                                                                                                                              for measuring breast gene
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                 to measuring gene expression
                                                                                                                                                                                                                                                                                                         development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
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                                                                                                                                                                                                                                                                                               non-carcinoma
                                                                                                                                                                                                                                                                                                                               expression
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RESULT 14
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Best Local Similarity
                                          04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234667P.
27-SEP-2000; 2000US-23559P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel single exon nucleic acid probes (see AII00010-AAII0067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, stagling, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases, proliferative
                                                                                                                                                                                                                                                                                                                            chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                WO200186003-A2
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG37017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                               30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                15-NOV-2001.
                                                                                                                                                                                                                                                                                                                hyaline membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG37017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSHLGTYY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKLSRALRYYYDKNIMTKYHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKLSRALRYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide encoded by genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                          single exon probe; asthma; lung cancer; COPD; ILD; c obstructive pulmonary disease; interstitial lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 11704; 322pp; English
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                                                                                                                                                                                                                                                                                                                disease.
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Pred. No. 3
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.2e-77;
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RESULT 15
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CC microarcis, pulmonary histocytosis, lymphangioleiomyontosis, pulmonary compression expression expression and for the supplemental pulmonary disease.

CC microarcis, pulmonary histocytosis, lymphangioleiomyontosis, compression expression expression expression expression expression expression expression expression expression express
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                  ABB31070 standard; Peptide; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12614 nucleic acid sequences mentioned in the specification, or the complements or the 12487 none recast - firm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                395
                                                                                                                                                                                                                                                                       335
                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                               DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYH 394
                                                                                                                                 AHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSHLGTYY
                                                                                                                                                                         AHPOKMNEVAPHPPALPVTSSSEFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY
                                                                                                                                                                                                                     DKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYH
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the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 3.2e-77;
4; Mismatches 4;
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                                                                                                                                                                                                                                                                                              Incleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                  Matches
                                                                                                                                                                Query Match
                                                                                                                                                                                                                            probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 14038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #3721 encoded by breast cell single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB31070;
                                 352
                                                                              292 LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT
 61
                                                                                                                                                  Local Similarity
                                                                  ب
                 KVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALP 411
KVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALP
                                                              LLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT
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                                                                                                                                                                                                   144 AA;
                                                                                                                                  Conservative
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
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                                                                                                                                               32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to a spatially-addressable set of single exon or measuring gene expression in a sample derived BT 474 cells. The method involves contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327pp + sequence listing; English.
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Pred. No. 1.7e-63;
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                                                                                                                                 Mismatches
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412

VTSSSFFAAPNPYWNSPTGGIYPN

121 VTSSSFFAAPNPYWNSPTGGIYPN 144

В

Search completed: November 9, 2002, 16:50:22 Job time : 55.4015 secs

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Result
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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16.4
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
   Match
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcstUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-878-177-1
US-08-767-93-6
US-08-767-93-6
US-08-767-93-6
US-09-750-580-1
US-07-853-913-3
US-09-780-175-96
US-08-904-032-2
US-08-991-789A-154
US-09-062-451-154
US-09-062-451-154
US-09-062-451-154
US-09-598-326-154
5171840-1
US-09-479-6-1
US-09-479-856-2
US-09-372-339-2
US-08-646-301A-1
US-08-647-958A-1
US-08-647-975A-1
US-08-647-339-2
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Patent No.
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Sequence 2
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PCT-US93-05704-1	US-08-063-552-1	US-08-969-106-9	US-09-113-426-1	US-09-351-198-1	US-08-188-275A-1	US-08-656-984A-33	US-09-522-217-106	PCT-US94-10358-7	US-08-889-108-7	US-09-134-078-8	US-08-993-581B-2	US-08-489-733-2	US-08-704-931-3	PCT-US91-03478-12	US-08-442-043A-12	US-08-091-519-12	US-09-144-367-3
Sequence 1, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 33, Appl	Sequence 106, App	Sequence 7, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 3, Appli

## ALIGNMENTS

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; TYPE: DNA; ORGANISM: C-11 gene, c-erg gene w/ US-08-878-177-1
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US-08-313-553-6
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Best Local S
Matches 18
                                                                                                                                                                                                                                     Sequence 6, Application US/08313553
Patent No. 5641650
GENERAL INFORMATION:
APPLICANT: TRINER, George J.
APPLICANT: BETLACH, MAIY C.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
TITLE OF INVENTION: IN HALOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: chugai seiyaku kabushiki kaisha 5001
CURRENT APPLICATION NUMBER: US/08/878,177
CURRENT FILLING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08878177 Patent No. 6294354 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwamoto et TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes TITLE OF INVENTION: the Proteins
                                                                                                                                          NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center
CITY: San Francisco
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            STREET: 4 | CITY: San | STATE: Cal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
OPERATING
SOFTWARE:
                                                                                           ZIP: 94111
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTCAGAGAGAGAGGAGCC 18
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18; Conserv
                                                                                                                              California
                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; 100.0%; Pred. No.
Release #1.0,
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                                                                                                                                                                 Center, Suite 3400
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Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Length 1447;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

FILING DATE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,553

Query Match Best Local Matches

Similarity

91.18; 94.48;

Score 16.4; Pred. No. 27; Mismatches

DB

Length 1956; Indels

0;

Gaps

0;

Conservative

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1 CTCAGAGAGAGAGGAGCC 18

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US-08-313-553-6
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NAME/KEY: misc_feature
LOCATION: 427..435
OTHER INFORMATION: /note
FEATURE:
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[NFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
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FEATURE:
NAME/KEY:
LOCATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                             LUCATION: replace(1863, "")
OTHER INFORMATION: /note= ",
OTHER INFORMATION: Alwni re.
Particle.
                                                                                                                                       NAME/KEY:
LOCATION:
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LOCATION:
              NAME/KEY: terminator LOCATION: 1813..1815
OTHER INFORMATION: /r
OTHER INFORMATION: cc
                                                                                                                                                                                                                                                             NAME/KEY: mutation
LOCATION: replace(1245, "")
OTHER INFORMATION: /note= "
OTHER INFORMATION: PstI res
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: replace(930, OTHER INFORMATION: /not OTHER INFORMATION: Alwi
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OTHER INFORMATION: /note= "G to T mutation removes
OTHER INFORMATION: AlwNI restriction site."
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LOCATION:
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LOCATION:
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OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Walter H. REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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376..1812
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376..414
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              /note= "Muscarinic "OM1" stop
codon."
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/note= "G to A mutation removes
AlwNI restriction site."
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PstI restriction site."
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codon."
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                                                                                                                                                                                            "RNA start site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "AlwNI cloning site."
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RESULT 3
US-08-767-993-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                              PEATURE:
NAME/KEY: terminator
LOCATION: 1864..1866
OTHER INFORMATION: /nc
OTHER INFORMATION: COC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1305 CTCAGAGGGAGAGGAGCC 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                  FEATURE:
                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 15
                                                                                                 NAME/KEY:
LOCATION:
               NAME/KEY:
                                                              LOCATION: replace(213, "")
OTHER INFORMATION: /note= "G to T mutation removes
OTHER INFORMATION: AlwNI restriction site."
                                                                                                                                                                                                                                    NAME/REY: misc_feature
LOCATION: 376..414
OTHER INFORMATION: /note= "Bacteriorhodopsin
OTHER INFORMATION: pre-sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1956 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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BETLACH, 1
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376..1812
                 misc_feature
427..435
                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                          linear
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Mary C.

EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
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                                                                                                                                                  /note= "codon."
 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/767,993
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                                                                                                                                                                "Bacteriorhodopsin stop
"AlwNI cloning site."
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RESULT 4
US-09-750-580-1
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                                                              PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
SEQ ID NO
LENGTH:
                                                                                                                                                                                                                                                                                                             APPLICANT: Salte
TITLE OF INVENTION FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FILE REFERENCE: 89.US2.CIP CURRENT APPLICATION NUMBER: US/09/750,580 CURRENT FILING DATE: 2000-12-28 PRIOR APPLICATION NUMBER: US 09/599,362 PRIOR FILING DATE: 2000-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
              SOFTWARE:
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LOCATION: replace(930, "")
OTHER INFORMATION: /note= "G to A mutation of the information alwni restriction site."
FEATURE:
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LOCATION: 1813..1815
OTHER INFORMATION: /note= "Muscarinic "OM1" stop
OTHER INFORMATION: codon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(1863, "")
OTHER INFORMATION: /note= "C to T mutation removes
OTHER INFORMATION: AlwNI restriction site."
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OTHER INFORMATION: /note= "T t
OTHER INFORMATION: AlwNI site.
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OTHER INFORMATION: /note= "
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                                                 OF SEQ ID NOS:
81001
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                                Patent.pm
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Ebbets-Reed, Dana
Salter-Cid, Luisa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bour, Barbara
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Pred. No. 2
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NAME/KEY: primer_bind
LOCATION: 1357. 1377
OTHER INFORMATION: 20-828.rp
NAME/KEY: primer_bind
LOCATION: 12029.12050
OTHER INFORMATION: 17-42.pu
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LOCATION: 45442
OTHER INFORMATION: 2
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 2
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LOCATION: 12347
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 1
                                                                                          NAME/KEY: primer_bind LOCATION: 45328..45347 OTHER INFORMATION: 20-
                                                                                                                                                                                        NAME/KEY: primer_bind LOCATION: 42070..42090 OTHER INFORMATION: 20-
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LOCATION:
   OTHER INFORMATION:
              NAME/KEY: primer_bind LOCATION: 76644..76664
                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 42572..4259
OTHER INFORMATION: 20
                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                       NAME/KEY: primer_bind LOCATION: 15460..15482
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 17-41.pu
                                                                                                                                                                                                                                                                                                   NAME/KEY: primer_bind LOCATION: 14992..15012
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LOCATION: 1239
OTHER INFORMATION:
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OTHER INFORMATION: exon
                                              OTHER INFORMATION:
                                                              NAME/KEY: primer_bind LOCATION: 45863..45883
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OTHER INFORMATION:
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LOCATION: 1427
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LOCATION: 10946..12946
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LOCATION: 42218
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                                              20-842.rp
                                                                                            20-842.pu
                                                                                                                                        20-841.rp
                                                                                                                                                                                        20-841.pu
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20-853.pu
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                                               complement
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US-07-853-913-3/c
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Best Local S
Matches 16
               Sequence 3, Application US/07853913 Patent No. 5338839 GENERAL INFORMATION:
                                                                                                                                              OTHER INFORMATION: 20-842-115.probe NAME/KEY: misc_binding LOCATION: 77046..77070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_binding
LOCATION: 12335.12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER_INFORMATION: 17-41-250.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
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LOCATION: 42219...42237
OTHER INFORMATION: 20-841-149.mis
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LOCATION: 42199..42217
OTHER INFORMATION: 20-
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LOCATION: 12348..12366
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OTHER INFORMATION: 17-42-319.mis
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LOCATION: 1240..1258
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OTHER INFORMATION: 20-828-311.mis
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 APPLICANT:
                                                                                                                                                                                  1 CTCAGAGAGAGAGGAGC 17
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                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                       Conservative
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Ronald D.G.
                                                                                                                                                                                                                                        85.6%;
94.1%;
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                           Score 15.4;
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RESULT 6
US-09-780-175-96/c
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                       APPLICANT: Robert McNay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
CURRENT FILING DATE: 2001-02-08
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Robert McKay
                                                                                                                                                                                                                        Sequence 96, Appli
Patent No. 6440738
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                TYPE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING LASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US 07/660,412
APPLICATION NUMBER: 22-FEB-1991
                                                                                                                                                                                                                                                                                                                               1239 CAGAGAGAGAGGAGC 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 07/503,000 FILING DATE: 25-CCT-1990 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: US 07/201,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07 FILING DATE: 02-JUN-1988 PRIOR APPLICATION DATA; APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lendahl, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 19920
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100.0%;
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Neuroepithelial Tumors
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Pred. No.
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; NAME/KEY:
; LOCATION:
US-08-651-579-1
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US-08-651-579-1/c
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                   Query Match
Best Local 9
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Best Local
   Best Local
Matches
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,579
FILING DATE: 22 MAY 1996
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-7401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                  TELEPHONE: (617) 227-7
TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION:
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LOCATION:
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LOCATION: (62)
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LOCATION:
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BROJATSCH, JURGEN
APPLICANT: NAUGHTON, JOHN
APPLICANT: YOUNG, JOHN A. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5597 CTCAGAGAGAGAGA 5583
                                                                                                           FEATURE:
                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TUMOR VIRUS SUSCEPTIBILITY GENES AND GENETITLE OF INVENTION: PRODUCTS, AND USES RELATED THERETO
                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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les 15; Conserv
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                                                                                                                                                                                  LENGTH:
 16; Conservative
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: CDS
: (4112)...(4150)
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                                                                                                                                                                                    2413 base pairs
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                                                                             CDS
215..1318
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              82.2%;
Score 14.8; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 2;
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1.3e+02;
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                            Length 2413;
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0;
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Gaps
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US-08-904-032-2/c
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                                                                  Sequence 10
Patent No.
GENERAL IN
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Patent No.
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
             APPLICANT:
APPLICANT:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                         APPLICANT:
                                                      APPLICANT:
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: EMBRYC
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                               1 CTCAGAGAGAGAGGAGCC 18
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 2, The
No. 600477
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                                                                                 10, Application US/08484044
5. 5552282
                                                                    INFORMATION:
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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           Fu, Ying-Hui
Friedman, David L.
Pizzuti, Antonio
Fenwick, Raymond G.
                                                     Caskey, C. T.
                                                                                                                                                                                                                                                                                                              BLADNOT 03
                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                2:
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                                                                                                                                                                                                                                        Score 14.8; DB 3; Pred. No. 1.5e+02;
                                                                                                                                                                                                                             Mismatches
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; MOLECULE TYPE:
US-08-484-044-10
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                                                                                                                                                                                                                                                                                                                                                           Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 154,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4318 CTCAGAGGAGGAGGAGGC 4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C
FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TELEFAX: 762829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTCAGAGAGAGAGGAGCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                       APPLICANT: Frudakis, Tony N. Smith, John M.
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: U.S.A.
77010-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                 ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                    ZIP: 98104-7092
                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
                                                                                                                                                                                                                                                                                                                                                                                            Application US/08991789A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fulbright & Jaworski, L.L.P.
)1 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                           Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/019,940
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                                                                                                                                                                                                                                                                          TREATMENT
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                        DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
L.6e+02;
hes 2;
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US-09-062-451-154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-991-789A-154
    Matches
                 Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 154,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 682-491
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                               STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                    NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-AP: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09062451
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
    Conservative
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Reed, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frudakis, Tony N.
                                                                                 linear
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04-APR-1997
                                                                                            single
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                 93.8%;
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    0;
Score 14.4; DB 4;
Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
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                                Length 345;
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   Indels
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RESULT 13
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                                                                                       5171840-1
                                                                                                                                                                                                         ;Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
;STIMULATORY FACTOR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-598-326-154
                                                                                                                       SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENCTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154, Application US/09598326 Patent No. 6423496 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                        NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                   133 CTCAGAGAGGAGGAG 148
                                                                                                     LENGTH:
                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                    1 CTCAGAGAGAGAGGAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: -UDMENOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
15; Conserv
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STATE: Washington
                                                                                                       2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Seed Intellectual Property Law Group PLLC STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                  Conservative
                                                                                                                                          19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed, Steven G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                80.0%;
93.8%;
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                                                                                                                                                        US/07/298,694
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                Score 14.4; DB 6;
Pred. No. 2.2e+02;
0; Mismatches 1;
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 345;
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RESULT 14
5480796-1
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US-08-795-473B-2
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TOPOLOGY: US-08-795-473B-2
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APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08795473B Patent No. 6217858
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NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                           TELEFAX: (212)-997-10
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/907,650
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212)-997-1028
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Davidson, Clifford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10
                                                                                                                                                                              NAME: Davidson, Clifford M. REGISTRATION NUMBER: 32,728 REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/795,473B FILING DATE: 11-FEB-1997
                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                          (212)-997-1037
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Pred. No. 2
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      Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/U
2: /cgn2_6/ptodata/1/pubpna/U
3: /cgn2_6/ptodata/1/pubpna/U
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19: /cgn2_6/ptodata/1/pubpna/U
10: /cgn2_6/ptodata/1/pubpna/U
11: /cgn2_6/ptodata/1/pubpna/U
12: /cgn2_6/ptodata/1/pubpna/U
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length	DВ	ID	Description
1	15.4	85.6	170	10	US-09-864-761-25721	Sequence 25721, A
2	15.4	85.6	401	10	US-09-960-352-966	
ω	15.4	85.6	506	10	US-09-917-800A-944	944,
4	15.4	85.6	583	10	US-09-864-761-9095	9095,
s	15.4	85.6	81001	10	US-09-751-877-1	1, App
6	15	83.3	171	10	US-09-878-574-5808	
7	15	83.3	258	10	US-09-563-817-31	
80	15	83.3	267	10	US-09-733-607-7	Sequence 7, Appli
9	15	83.3	272	10	US-09-878-574-7091	Sequence 7091, Ap
c 10	15	83.3	283	10	US-09-878-574-11646	٠,
c 11	15	83.3	481	10	US-09-864-761-11469	Sequence 11469, A
c 12	15	83.3	547	10	us-09-924-401-19	Sequence 19, Appl
13	15	83.3	5540	10	US-09-960-253-74	Sequence 74, Appl
14	14.8	82.2	183	10	US-09-867-701-8586	Sequence 8586, Ap
15	14.8	82.2	236	10	US-09-960-352-12042	Sequence 12042, A
16		82.2	297	10	US-09-867-701-1009	Sequence 1009, Ap
		82.2	507	10	US-09-867-701-988	Sequence 988, App
c 18	14.8	82.2	597	10	US-09-833-381-360	-
c 19	14.8	82.2	1530	10	US-09-989-002-1	1, A

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
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80.0	80.0	80.0	80.0	80.0		80.0				80.0	80.0	80.0	80.0	80.0	80.0	80.0	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	
888	603	559	493	479	479	461	429	401	401	357	345	345	271	269	241	241	302250	174424	167343	167343	13747	2910	2615	2229	
9	10	10	9	10	10	10	10	10	10	10	10	10	10	10	12	10	10	10	10	10	10	10	12	10	
US-09-938-842A-2493	US-09-974-300-6166	US-09-864-761-9133	US-09-978-295A-291	US-09-864-761-17297	US-09-864-761-501	US-09-728-445-14	US-09-878-574-3246	US-09-795-686-733	US-09-795-668-733	US-09-834-975-422	US-09-429-755-154	US-09-810-936-154	US-09-878-574-8668	US-09-878-574-12677	US-10-007-805-346	US-09-604-287A-346	US-09-962-832-154	US-09-967-768A-314	US-09-964-824A-273	US-09-962-436-281	US-09-964-824A-287	US-09-989-002-10	US-10-052-586-523	US-09-822-830A-143	00 00 000 000
Sequence 2493, Ap	Sequence 6166, Ap	Sequence 9133, Ap	Sequence 291, App	17297	501					Sequence 422, App	Sequence 154, App	Sequence 154, App		1267	346,	346	154,	Sequence 314, App	273	281		10,	Sequence 523, App	Sequence 143, App	date to a nonemboo

## ALIGNMENTS

RESULT 1 US-09-864-761-25721

; Sequence 25721, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION; APPLICANT: Penn, Sharron G.; APPLICANT: Rank, David R.; APPLICANT: Hanzel, David K.; APPLICANT: Chen "APPLICANT: Chen" PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB'24263.6
PRIOR APPLICATION NUMBER: GB'24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662 FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30

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OTHER INFORMATION: MAP TO AC007539.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.9

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BEAUTH SIGNAL = 3.4

OTHER INFORMATION: SWISSPROT HIT: BF124974.1, EVALUE 3.70e-02

OTHER INFORMATION: SWISSPROT HIT: P40024, EVALUE 7.80e-01
RESULT 3
US-09-917-800A-944
; Sequence 944, Application US/09917800A
; Patent No. US20020119462A1
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                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bos taurus ; OTHER INFORMATION: Clone ID: 05-LIB188-020-Q1-E1-B1 US-09-960-352-966
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/70/960,352

CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 966
                                                                                                                                                                                                                                                         Matches
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-864-761-9095
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9095, Application US/09864761 Patent No. US20020048763A1
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                                                                                 PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TILE REFERENCE: Aconica-X-1
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR FILING DATE: 2001-05-15 PRIOR APPLICATION NUMBER: US 60/292,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR FILING DATE: 2000-11-02 PRIOR FILING DATE: 2001-05-11 PRIOR FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038-US CURRENT EPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31
                                            PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
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                       APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/298,884
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Castle, Arthur
Elashoff, Michael
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2000-09-
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94.1%;
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Pred. No. 1
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RESULT 5
US-09-751-877-1
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Best Local Similarity
"hes 16; Conserv
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APPLICANT:
APPLICANT:
                     APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US3.REG
CURRENT APPLICATION NUMBER: US/09/751,877
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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OTHER INFORMATION:
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OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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NO 1
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00667
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              Patent.pm
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Dumas Milne Edwards,
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94.1%;
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Pred. No. 1.
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IN BONE MARROW, SIGNAL = 7.
IN FETAL LIVER, SIGNAL = 7.
IN ADULT LIVER, SIGNAL = 9.
IN BRAIN, SIGNAL = 3.9
IN HELA, SIGNAL = 4.6
IN PLACENTA, SIGNAL = 7.4
IN HEART, SIGNAL = 3.4
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NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp c
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
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LOCATION: 1239
OTHER INFORMATION: 2
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 1
               NAME/KEY:
LOCATION:
                                           OTHER INFORMATION: 20-
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-
                                                                                                    NAME/KEY: primer_bind LOCATION: 45328..4534
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LOCATION: 42572..42591
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LOCATION: 45442
OTHER INFORMATION:
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LOCATION: 15241
OTHER INFORMATION:
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LOCATION: 14271..15968
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 12947..12
OTHER INFORMATION:
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LOCATION: 929..949
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 15969..17969
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LOCATION: 13470..13526
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               primer_bind
76644..76664
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20-853.pu
                                            20-842.
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RESULT 6
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                    Sequence 5808, Application US/09878574 Patent No. US20020110548A1
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                         Matches
                                                                                                                                          47018
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NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
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LOCATION: 12335.12359
OTHER INFORMATION: 17-42-319.probe
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LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
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LOCATION: 42219. 42237
OTHER INFORMATION: 20-841-149.mls
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LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
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LOCATION: 45443..45461
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LOCATION: 45423..45441
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LOCATION: 12348..12366
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NAME/KEY: primer_bind
LOCATION: 1220..1238
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LOCATION: 42199..42217
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                                                                                                                                                              1 CTCAGAGAGAGAGGAGC 17
                                                                                                                                          CTCAGAGAGAGATGAGC 47034
                                                                                                                                                                                                                                                                                                                       20-853-415.probe
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94.1%;
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RESULT 8
US-09-733-607-7
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Best Local Similarity
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                                                                                                                                                                                           ; Sequence 7, Application US; Patent No. US20020042054A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : NUMBER OF SEQ ID NO
: SOFTWARE: FastSEQ f
: SEQ ID NO 31
: LENGTH: 258
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; OTHER INFORMATION: Clone ID: 701097386H1
US-09-878-574-5808
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER: OF SEQ ID NOS: 15775
SEQ ID NO 5808
LENGTH: 171
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Cirelli, Chiara
APPLICANT: Shaw, Paul J.
APPLICANT: Shaw, Paul J.
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Vigilance Nucleic Acids and Related
TITLE OF INVENTION: Diagnostic, Screening and Therapeutic
FILE REFERENCE: P-NI 4447
CURRENT APPLICATION NUMBER: US/09/733,607
CURRENT FILING DATE: 2001-09-10
                                                                                                  APPLICANT: Tononi, Giulio
APPLICANT: Cirelli, Chian
APPLICANT: Shaw, Paul J.
APPLICANT: Greenspan, Rai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/563,817
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR FILING DATE: 1999-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nehls, Michael C.
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020095031A1el
TITLE OF INVENTION: Polypeptides Encoded
FILE REFERENCE: LEX-0021-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: homo sapiens
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Pred. No.
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; SEQ ID NO 7091
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701099415H1
US-09-878-574-7091
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; ORGANISM: Drosophila
US-09-733-607-7
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SEQ ID NO 11146

LENGTH: 283

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 701064705H1
3-09-878-574-11646
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                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                   PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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                                                                                                                                                                                                                                                                       APPLICANT: Byrum, Joseph R.
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR ETLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
DELIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                OTHER INFORMATION:
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                                                                                OTHER INFORMATION:
                                                                                                    OTHER INFORMATION: MAP TO AC006065.3
                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                 ENGTH:
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
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IN FETAL LIVER, SIGNAL = 0.81
IN BAAIN, SIGNAL = 0.65
IN BONE MARROW, SIGNAL = 0.74
IN ADULT LIVER, SIGNAL = 1
IN PLACENTA, SIGNAL = 0.71
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Pred. No.
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                                                                                                                 ; TYPE: DNA; ORGANISM: Homo sapiens US-09-960-253-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = US-09-864-761-11469
                                                                                                                                                                                                                                                                                                                                                                                       US-09-960-253-74
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Matches
                                                                       Query Match
Best Local :
                                                                                                                                                                            SOFTWARE: FastSEQ
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 85
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 547
                                                         Matches
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 74, Application US/09960253 Patent No. US20020123619A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09924401 Patent No. US20020142957A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                  APPLICANT: Benson, Darin R.
APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIANGOSIS OF COLON CANCER FILE REFERENCE: 210121.550
CURRENT APPLICATION NUMBER: US/09/924,401
CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
                                                                                                                                                            LENGTH: 5540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
2157 TCAGAGAGAGGAG 2171
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nes 15; Conserv
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100.0%; Pr
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Pred. No.
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Pred. No.
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Pred. No.
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                                                                    DB 10; 1
2.2e+02;
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1.8e+02;
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APPLICANT: Warren, Wesley C.
APPLICANT: Marien, Wesley C.
APPLICANT: Mathalagan, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-99-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12042
LENGTH: 236
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 51-LIB34-068-Q1-E1-E4
US-09-960-352-12042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8586
LENGTH: 183
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-8586
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Best Local Similarity
Whiches 16; Conserve
Search completed: November Job time: 16.4007 secs
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Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aplate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12042, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
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                                                                 206 CTCATGGAGAGGAGGCC
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88.9%;
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Pred. No. 2.1e+02;
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Pred. No. 2
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Maximum Match 100%
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2: /SIDSZ/gcgdata/g
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4: /SIDSZ/gcgdata/g
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Copyright (c) 1993 - 2002 Compugen Ltd
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esult No.	Score	% Query Match	Query Match Length DB	DB	Ħ	Description
_	18	100.0	1447	20	AAX26551	DNA encoding chic
2	16.4	91.1	1422	23	ABI97996	Non-endogenous hu
ω	16.4	91.1	1522	21	AAF21022	Human low adenosi
4	16.4	91.1	1522	21	AAA34900	Human adenosine r
<sub>5</sub>	16.4	91.1	1956	15	AAQ73587	Fragment of the m
6	16.4	91.1	2100	22	AAS02501	Human gene for m1
7	16.4	91.1	2100	22	AAS02502	Human gene for ml
8	16.4	91.1	2100	22	AAS02503	Human gene for m1
9	16.4	91.1	2100	22	AAS02504	Human gene for m1

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		15.4 15.4 15.4 15.4	<b>⊢</b>
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	22 22 23 24	222	110 110 110 110 110 110 110 110 110 110
ABA63430 ABA30629 AAK11963 AAK37668 AAK18425 AAI18425 AAI43541 ABS11656	AA156489 ABS23978 AAK81511 AAK81512 AA182088 ABV48538 ABV48538	ABN30396 ABA75834 ABA40401 AAK24515 AAK50504 AAI27517	AAS02505 AAS02508 AAS02508 AAG02068 AAG02068 AAN92068 AAN92068 AAR926690 AAF74417 ABK64512 AAF74417 ABK64512 AAF344672 AAS94851 AAF31026 AAF32303 AAF22303 AAK846996
an foetal be #9095 f an brain e an bone ma bo #8358 f be #8327 an genome-	#25175 used genome-deri immune/haem immune/haem polynucleot prostate ex equence diff	pliced t foetal #18867 brain e bone ma #17450	n gene for ml n gene for ml n gene for ml n gene for ml n muscarinic n muscarinic tate cancer-a cotide sequen ue remodeling n cDNA differ n benign pros n full-length n DNA sequenc n low adenosi n adenosine r idopsis thali n immune/haem

## ALIGNMENTS

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Chicken; C-11 protein; cell calcification inhibiting activity; cell calcification inhibiting agent; c-erg protein; arthritis deformans; ossification; spinal column ligament; ss.
                                  20-JUN-1997;
18-JUN-1997;
                                                                                                                                               Gallus
                                                                                                                                                                                                 DNA encoding chicken C-11 protein.
                                                                                                                                                                                                                  14-JUN-1999 (first entry)
                                                                                                                                                                                                                                     AAX26551;
                                                                                                                                                                                                                                                     AAX26551 standard; DNA; 1447
                                                                           23-MAR-1999
                                                                                            JP11075871-A.
         (CHUS ) CHUGAI PHARM CO LTD (UYPE-) UNIV PENNSYLVANIA.
                                                           29-MAY-1998;
                                                                                                                                               sр
                                  97US-0050297.
97US-0878177.
                                                          98JP-0166076
                                                                                                            /*tag=
                                                                                                                      Location/Qualifiers 63..1418
                                                                                                                                                                                                                                                      BP.
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WPI; 199

1999-257708/22. DB; AAY01520.

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RESULT 2
ABI97996
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Best Local S
Matches 18
                                  the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disor associated with GPCRs. The present sequence encodes a non-endogenous control of the 
                                                                                                                                                                                                                                                                               Identifying agonists of G disease treatment, comprise
                                                                                                                                                                                                                  Example 2; Page 312;
                                                                                                                                                                                                                                                             versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2001; 2001WO-US11098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABI97996 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                  Lehmann-Bruinsma K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177172-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constitutively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABI97996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a chicken C-11 protein which has cell calcification inhibiting activity. The specification also describes a cell calcification inhibiting agent containing c-erg protein (AAY01521). The proteins are used for measuring the calcification of a (CAAY01521) for diagnosing arthritis deformans or ossification of spinal column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                      2001-648759/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGAGAGAGAGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGAGAGAGAGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                    ABB56360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor; GPCR; non-endogenous;
tively activated GPCR; agonist; disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein for inhibiting cell calcification the calcification of a cell, for diagnosing or ossification of spinal column ligament
                                                                                                                                                                                                                                                             GPCRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-195747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                      relates to G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 A; 374 C; 317 G;
             human GPCR
                                                                                                                                                                                                                                                                               comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPCR
                                                                                                                                                                                                               394pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  Liaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                               protein-coupled receptors (GPCRs)
ses contacting candidate compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                      receptors (GPCRs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512.
                                      encodes a non-endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant;
                                                             disorders
                                                                                                                                                                                                                                                                                  with
                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                             the
                                                                                                                                                                         for which
                                                                                                                                                                                                                                                                                                      use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 3
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                                     oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                     trigger
cancers
                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1422 BP;
                                                                                                                                                                                                                                                                                                                                                                                                               Nyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF21022 standard;
                             transmitters, defensins, growth factors, vasoactive peptides and
                                                                                                                                                                                                                                                            The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000WO-US08020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200062736-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2001
              receptors,
                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which
                                                                                                                                                                                                                                                                                                                                                                                                                                          (NYCE/) NYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYEC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pulmonary hypertension; emphysema; pulmonary transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lmmunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               low adenosine antisense oligonucleotide; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTCAGAGAGAGAGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                 2000-679539/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV EAST CAROLINA NYCE J W.
                                                                                                                                                                                                                                                                                                                     obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
, binding proteins and malignancy associated oligonucleotides may be used in this way to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenosine
                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127958
                                                                                                                                                                                                                                                                                     832-833; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 482
                                                                                                                                                                                                                                                          describes low adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligonucleotide related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 T; 0 other;
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                                                                                                                                                                                                                                                         (A) content antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
            proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence #2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergy;
                                                                                                                                                                                                                                                                                                                                                   do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection;
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RESULT 4
AAA34900
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alivays, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                   New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                   Nyce
                                                                                                                                                                                                                                                                                                                                               03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenosine receptor related polynucleotide SEQ ID NO:2589
                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                              (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200009525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA34900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA34900 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(les) and/or surfactant hypoproduction which are associated with a disease
                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAGAGAGAGAGGAGCC
                                                                                                                                                                                                                                                  2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGAGGGAGAGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenosine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia;
                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                               9805-0095212
                                                                                                                                                                                                                                                                                                                                                                              99WO-US17712
                                                                                                                                         762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.18;
94.48;
                                                                                                                                        1343pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.6
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4;
                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
. 2.6e+02;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
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RESULT 5
AAQ73587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        뭥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, CC carcinomas, and cancers which may metastasise to the lungs, including CC breast and prostate cancer. The reduction of the adenosine content of CC the ONs reduces side effects. The A-containing ONs break down with the CC release of deoxyadenosine which activates adenosine receptors causing CC concloconstriction and inflammation. AAA32313 to AAA35312 represent the CC nucleotide sequences given in the sequence listing from the present CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last CC 185 sequences are also called SEQ ID NO:1 to 2815, and then the previously named sequences. SEQ ID NO:11 to 1680 CC (AAA32323 to AAA3392) are specifically claimed ONs from the present CC invention. N.B. Sequences given in the disclosure of the present CC invention do not match up with their corresponding SEQ ID NO:: sequences given in the sequences sequences is the present CC invention do not match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                         Expression of heterologous proteins in halo-bacteria - using regulatory and stop sequences from halo-bacteria, pref. the bacterio-rhodopsin gene.
                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                  Disclosure;
                                                                                                                                                                                                                  Betlach MC,
                                                                                                                                                                                                                                                                        25-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment of
                                                                                                                                                                                      WPI; 1994-317010/39.
                                                                                                                                                                                                                                                                                                                                                              WO9421789-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ73587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ73587 standard; DNA; 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1522
                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                       28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                   29-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAGAGAGAGAGGAGCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAGAGGGAGAGGAGCC 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conser
                                                                                                                                                                          AAR60695
                                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                  Turner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 301 A; 520 C; 413 G;
                                                                                                                                                                                                                                                                          93US-0038662
                                                                                                                                                                                                                                                                                                       94WO-US02388
                                                                                 6; 118pp;
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 376..1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
                                                                                                                                                                                                                    GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                            D)
                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.4; DB 2: Pred. No. 2.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0

The sequence is that of the human muscarinic acetylcholine receptor gene fragment. The gene is used to exemplify a new expression vector for producing heterologous polypeptides in

halobacterial

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RESULT 6
AAS02501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS X
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                            exon
New variants of the ml muscarinic acetylcholine receptor gene, useful
                                 Choi JY,
                                                                        12-OCT-2000; 2000WO-US28211
                                                                                      19-APR-2001
                                                                                                   WO200127312-A2.
                                                                                                                             intron
                                                                                                                                                 variation
                                                                                                                                                                    variation
                                                                                                                                                                                        variation
                                                                                                                                                                                                            variation
                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                Human; ml acetylcholine receptor; CHRM1; immunogen; antibody; Alzheimer's disease; dementia with Lewy bodies; DLB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                            1305 CTCAGAGGAGGAGGAGCC 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1956 BP; 394 A; 635 C; 545 G; 382 T; 0 other;
                                                                                                                                                                                                                              variation
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    Human gene
                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                              AAS02501;
                                                                                                                                                                                                                                                                                                                                                                                           AAS02501 standard;
                                              (GENA-)
                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTCAGAGAGAGAGGAGCC 18
             2001-282046/29.
DB; AAU01293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                              GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                Denton RR,
                                                                                                                                                                                                                                                                                                                                                    for m1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                            99US-0159269
                                                                                                                           /"Lay= n
/label= "Single_nucleotide_polymorphism"
1834..2100
                                                                                                                                                                                                                                                                     /number= 1
451..1833
/*tag= b
                                                                                                                                                replace
                                                                                                                                                                                                                             /note= "This CDS replace (717,A)
                                                                                                                                                                    replace
                                                                                                                                                                                       /label= "Single_nucleotide_polymorphism"
replace (1233,T)
                                                                                                                                                                                                          /label= "Single_nucleotide_polymorphism"
replace (1199,A)
                                                                                                                'number=
                                                                                                                                                       /label=
                                                                                                                                                                                                                                           /product= "CHRM1
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                        51..1833
                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor, CHRM1.
                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.1%;
                                Nandabalan
                                                                                                                                                                                                                                                                                                                                                                                            2100
                                                                                                                                                                   "Single_nucleotide_polymorphism" (1494,A)
                                                                                                                                               "Single_nucleotide_polymorphism"
(1803,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.4;
Pred. No. 2
                                                                                                                                                                                                                                   protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                ~
                                                                                                                                                                                                                                   specifically claimed"
                                Stephens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                          RESULT 7
AAS02502
ID AASC
 뮹
                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 17
12-OCT-2000; 2000WO-US28211
            19-APR-2001
                                                                                                                                         CDS
                                                                                                                                                             exon
                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                               AAS02502;
                          WO200127312-A2
                                                    intron
                                                                       variation
                                                                                           variation
                                                                                                               variation
                                                                                                                                                                                intron
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                 29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                Sequence 2100 BP; 458 A;
                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                       | Similarity
17; Conserv
                                                                                                                                                                                                                                    for
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to find treatment for Alzheimer's and dementia, have single nucleotide variations at one or more of five polymorphic sites {\tt -}
Claim 1; Fig 1; 52pp; English.
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The sequence represents the Human gene encoding the ml muscarinic acetylcholine receptor, CHMR1. CHMR1 is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, mAChR, that play important roles in higher brain function such as learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are useful for diagnosing and developing treatments for diseases associated useful for diagnosing and developing treatments for diseases associate with the abnormal expression of the gene or activity of the protein, Alzheimer's disease and dementia with Lewy bodies.

Note: The present sequence also represents haplotype 6, as detailed in table 4 (page 31) of the specification. 663 C; 571 G; 408 T; 0 other; e.g.

1320 CTCAGAGGAGAGAGCC 1337 1 CTCAGAGAGAGAGGAGCC 18 Conservative 91.18; 0 Score 16.4; Pred. No. 2 Mismatches 6e+02; DB 22; Indels Length 2100; 0;

Gaps

0;

Human; m1 acetylcholine receptor; CHRM1;
Alzheimer's disease; dementia with Lewy b AAS02502 standard; DNA; 2100 BP (first entry) ml muscarinic acetylcholine receptor, ; immunogen; antibody; bodies; DLB; haplotyp haplotype 1; haplotype

/product= "CHRM1 | /note= "This CDS replace (717,C) /number= 1 451..1833 /\*tag= b /label= "Single\_nucleotide\_polymorphism"
replace (1199,G) replace /number= 1 451..1833 /label= "Single\_nucleotide\_polymorphism" 1834..2100 Location/Qualifiers /\*tag= /label= \*tag= /\*tag= ..450 þ "Single\_nucleotide\_polymorphism" (1803,C) protein"
is specifically claimed"

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RESULT 8
AAS02503
          밁
                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                        acetylcholine receptor, CHMR1, haplotype 1. CHMR1 is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, mAChR, that play important roles in higher brain function such as learning and memory. The protein is a possible drug target for treatment for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and adveloping treatments for diseases associated with the abnormal expression of the gene or activity of the protein, e.g Alzheimer's disease and dementia with Lewy bodies.

Note: The present sequence is not shown in the specification but is derived from the CHMR1 sequence given in AASO2501 and information contained in table 4 (page 31) of the specification.
                                                                                                                                                                                                                                                                                                                    1320
                                                                                                                   exon
                                                                                         CDS
                                                                                                                                                      Key
                                                                                                                                                                       Homo
                                                                                                                                                                                                                   Human gene
                                                                                                                                                                                                                                    29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the ml muscarinic acetylcholine receptor gene, useful to find treatment for Alzheimer's and dementia, have single nucleotide variations at one or more of five polymorphic sites -
                           variation
                                                     variation
                                                                                                                                             intron
                                                                                                                                                                                        Alzheimer's
                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                      AAS02503;
                                                                                                                                                                                                                                                                        AAS02503 standard; DNA; 2100 BP
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 26; Page - ; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents the Human gene encoding the ml muscarinic
                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                   CTCAGAGGGAGGAGGCC 1337
                                                                                                                                                                                                                                                                                                                                    CTCAGAGAGAGAGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-282046/29.
                                                                                                                                                                                                  己
                                                                                                                                                                                                                                                                                                                                                       17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           2100 BP;
                                                                                                                                                                                      acetylcholine receptor; CHRM1; immunogen; acetylcholine receptor; CHRM1; immunogen; as disease; dementia with Lewy bodies; DLB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denton RR,
                                                                                                                                                                                                                 for ml muscarinic acetylcholine receptor, haplotype
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                    (first entry)
                                                  /product= "CHRM1 |
/note= "This CDS replace (717,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159269.
                                                                                      /*tag= b
/number= 1
451..1833
                                                                                                                  /number= 1
451..1833
                          /label= "Single_nucleotide_polymorphism"
replace (1803,C)
                                                                               /*tag= c
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         460 A;
                                                                                                                                                                                                                                                                                                                                                              91.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nandabalan
                                                                                                                                    D)
e
"Single_nucleotide_polymorphism"
                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                          661 C;
                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                      Score 16.4; In Pred. No. 2.6e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          570 G;
                                                             protein" is speci:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                            specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stephens
                                                                                                                                                                                                                                                                                                                                                                                          409 T;
                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                               antibody;
                                                                                                                                                                                       haplotype 2;
                                                                                                                                                                                                                                                                                                                                                                        2100;
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatments
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g
                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                              RESULT 9
AAS02504
                                                                                                                                                                                                                                                                                                          SXCCCCCCCCCCCX PX PT TX X X X X X X X X X X Y T T T
       밁
                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                              Query Match
Best Local
       CDS
                                 exon
                                                                                      Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi JY,
                                                                                                                                                                      AAS02504;
                                                                                                                                   Human
                                                                                                                                                    29-AUG-2001
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-2001
                                                            intron
                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                     Н
                                                                                                                                  gene
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1320 CTCAGAGGGAGAGGAGCC 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acetylcholine receptor, CHMR1, haplotype 2. CHMR1 is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, maChR, that play important roles in higher brain function such as learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are useful for diagnosing and devileng treatments for diseases associated with the abnormal expression of the gene or activity of the protein, e.g. Alzheimer's disease and dementia with Lewy bodies.

Note: The present sequence is not shown in the specification but is
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                                                                                                                                                                                         Human; m1 acetylcholine receptor; CHRM1; immunogen; antibody;
Alzheimer's disease; dementia with Lewy bodies; DLB; haplotype 3;
                                                                                                                                                                                                                                                                                                                                                                                                            AAS02504 standard; DNA; 2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from the CHMR1 sequence given in AAS02501 an contained in table 4 (page 31) of the specification.
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                                                                                                                                                                                                                                                                 ml muscarinic acetylcholine receptor, haplotype
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Pred. No. 2.
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RESULT 10
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   Human;
                                                                                                                                                                     1320 CTCAGAGGGAGAGGAGCC 1337
                                                                                                                                                                                                                                                                                            useful for diagnosing and developing treatments for diseases associated with the abnormal expression of the gene or activity of the protein, e.g. Alzheimer's disease and dementia with Lewy bodies.

Note: The present sequence is not shown in the specification but is derived from the CHMR1 sequence given in AASO2501 and information contained in table 4 (page 31) of the specification.
                                                                                                                                                                                                                                                                                                                                                                      acetylcholine receptor, CHMR1, haplotype 3. CHMR1 is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, mAChR, that play important roles in the protein function such as learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are
                          Human gene
                                                    29-AUG-2001
                                                                              AAS02505;
                                                                                                       AAS02505 standard;
                                                                                                                                                                                                                                                                        Sequence 2100 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the ml muscarinic acetylcholine receptor gene, useful to find treatment for Alzheimer's and dementia, have single nucleotid variations at one or more of five polymorphic sites
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acetylcholine receptor; CHRM1;
                         for m1 muscarinic acetylcholine receptor, haplotype 4.
                                                                                                                                                                                                                       Conservative
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replace (1233,C)
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replace (1803,C)
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94.4%;
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                                                                                                                                                                                                                                                                       410 T; 0 other;
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immunogen; antibody;
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RESULT 11
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                                                                                                                                                                                                 learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are useful for diagnosing and developing treatments for diseases associated with the abnormal expression of the gene or activity of the protein, e.g. Alzheimer's disease and dementia with Lewy bodies. Note: The present sequence is not shown in the specification but is derived from the CHMR1 sequence given in AASO2501 and information contained in table 4 (page 31) of the specification.
                     AAS02506 standard;
                                                                                                                                                                                                                                                                                                           acetylcholine receptor, CHMR1, haplotype 4. CHMR1 is one subtype of family of 5 genetically distinct muscarinic acetylcholine receptors, mAChR, that play important roles in higher brain function such as
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                                                                                                                                                                                                                                                                                                                                                                                                New variants of the ml muscarinic acetylcholine receptor gene, useful to find treatment for Alzheimer's and dementia, have single nucleotide variations at one or more of five polymorphic sites
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les 17; Conserv
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                                                                                                                                                                               2100 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denton RR,
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is specifically claimed"
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Note: The present sequence is not shown in the specification but is derived from the CHMR1 sequence given in AASO2501 and information contained in table 4 (page 31) of the specification.
                                                                                                                                                                                           acetylcholine receptor, CHMR1, haplotype 5. CHMR1 is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, mAChR, that play important roles in higher brain function such as learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are not polypeptide.
                                                                                                                                                                                                                                                                                                Claim 26; Page - ; 52pp;
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to find treatment for Alzheimer's
variations at one or more of five
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Alzheimer's disease; dementia with Lewy bodies; DLB; haplotype 5;
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/label= "Single_nucleotide_polymorphism"
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94.48;
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                                              Pred. No. 2.600; Mismatches
                                                          Score 16.4; DB 22;
Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                      acetylcholine receptor gen and dementia, have single polymorphic sites -
                                                                                                                                                                                                                                                                                                                                                                                                             Stephens JC;
                                                                                               408 T; 0 other;
                                                                     Length
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AAS02508
ID AAS
RESULT 12
                   acetylcholine receptor, CHMRI, haplotype 7. CHMRI is one subtype of a family of 5 genetically distinct muscarinic acetylcholine receptors, maChR, that play important roles in higher brain function such as learning and memory. The protein is a possible drug target for treatments for Alzheimer's disease and dementia with Lewy bodies (DLB). The gene, polypeptide, haplotypes and antibodies raised against the protein are useful for disquesting and developing treatments for diseases associated with the abnormal expression of the gene or activity of the protein, e.g. Alzheimer's disease and dementia with Lewy bodies. Note: The present sequence is not shown in the specification but is derived from the CHMRI sequence given in AASO2501 and information contained in table 4 (page 31) of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                               The sequence represents the Human gene encoding the ml muscarinic
                                                                                                                                                                                                                             New variants of the ml muscarinic acetylcholine receptor gene, useful to find treatment for Alzheimer's and dementia, have single nucleotide variations at one or more of five polymorphic sites
                                                                                                                                                                                                        Claim 26; Page - ; 52pp; English.
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Query Match Best Local Similarity

Score Pred. Ç

No.

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Length 2100

Sequence

2100 BP; 458 A; 662

571 G;

409 T; 0 other;

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Local Similarity nes 17; Conserv

Conservative

94.48;

Pred. No. 2.7 0; Mismatches

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 Query Match
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                                                                                                        diagnostic use. The genes are cloned by screening a rat cerebral cortex cDNA library with a probe based on nucleotides 170-225 of the non-coding strand of porcine brain (ml) cDNA (modified at positions 5, 38 and 53); identifying cDNA clones by hybridisation with BamHI or XhoI digests of plasmid DNA from 12 cultures contg. up to 500000 independent clones; reculturing until a pool contg. less than 5000 independent clones with a single hybridisation band are identified, and isolating individual clones by colony hybridisation.

Stable cell lines are produced by transfecting Chinese hamster ovary cells (CHO-KI) with various pCD vectors contg. the gene inserts.

See also AAQ02068-Q020671 and AAQ00086.
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                                                      granted patent numbers.
web site at www.derwent
                            Sequence 2880
                                                                (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent
                                                                                                                                                                                                                                              The sequence may be useful for synthesis of hybridisation probes for diagnostic use. The genes are cloned by screening a rat cerebral cor
                                                                                                                                                                                                                                                                                      The sequence was indexed from the best available specification
                                                                                                                                                                                                                                                                                                                   Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                           Cloned genes for muscarinic acetylcholine receptors for drug screening and diagnostic use.
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18-FEB-1999
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                                                                                                                                                                                                                                                                         dentifiable bases were annotated as 'N'
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                                                    www.derwent.com/dwpi/updates/ntis_us.html.)
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                           618 A; 921 C; 763
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reculturing until a pool conty. Less than 5000 indep. clones with a single hybridisation band are identified, and isolating individual clones by colony hybridisation.

Stable cell lines produced by transfecting Chinese hamster ovary cells (CHO-K1) with various pCD vectors conty. the gene inserts.

See also AAQ02068-0020671 and AAQ00086.

(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
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                                                                                                                                                                                                                                             The sequence may be useful for synthesis of hybridisation probes for diagnostic use. The genes are cloned by screening a rat cerebral cortex cDNA library with a probe based on nucleotides 170-225 of the non-coding strand of porcine brain (m1) cDNA (modified at positions 5, 38 and 53); identifying cDNA clones by hybridisation with BamHI or XhoI digests of plasmid DNA from 12 cultures contg. up to 500000 independent clones; reculturing until a pool contg. less than 5000 indep. clones with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloned genes for muscarinic acetylcholine receptors for drug screening and diagnostic use.
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                                           The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in comprise contact and are derived from the tissues of various corganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating compostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for contentifying modulators of prostate cancer or agents that inhibit compostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABS92115 ABS92263 represent prostate cancer-associated polynucleotide
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08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

06-APR-2001;
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30-APR-2001;
04-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 425-426; 436pp; English
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REFERENCE AUTHORS

Iwamoto,M., Higuchi,Y.,

Koyama, E.,

Enomoto-Iwamoto, M., Kurisu, K.,

KEYWORDS SOURCE ORGANISM

Gallus gallus.
Gallus gallus.
Eukaryota; Metazoa; Cl
Archosauria; Aves; Nec
Phasianinae; Gallus.
1 (bases 1 to 1413)

Neognathae;

Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae;

ACCESSION VERSION

AY065661.1

GI:17887440

AY065661 Gallus ga spliced. AY065661

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1413 bp mRNA line isoform C-1-1 mRNA, complete

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RESULT 1
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SUMMARIES

## Result No. 0 0 000 O O a 000 Score Query + 00 94.4.4 94.4 155816 165269 171111 181739 192095 195434 209384 209384 229687 239598 2395746 Length DВ 10 HSHM1 HSMIMAR HSMIMAR BC007740 BC022984 CBU42983 GC0022984 CBU4983 HUMFWRAS AX083652 HSFWRA AX281697 BC008786 DC008786 DC067939 AX059518 AC120154 AC120154 AC120154 AC118651 AC0194455 AC099145 AC118263 AC139952 AC139952 AC1997081 AC1097081 AC1027064 AC117064 AC0116059 AP002781 AC116059 AP002781 AC127313 ALIGNMENTS AC067939 Neurospor AX059518 Sequence AC100995 Mus muscu AC120154 Mus muscu AC124292 Homo sapi AC118651 Homo sapi AC014455 Homo sapi AC009142 Rattus no AC108282 Rattus no E31253 Protein hav AC018539 Homo sapi AC080023 Homo sapi AC18263 Mus muscu AC130907 Rattus no AC120952 Rattus no AC120958 Rattus no AC097081 Rattus no AC0107108185 Fells cat AC102702 Mus muscu AC117164 Rattus no AC102702 Mus muscu AC017064 Rattus no AC106059 Rattus no AC116059 Rattus nuscu AC127339 Mus muscu AX083652 Sequence X06256 Human mRNA AX281697 Sequence BC008786 Homo sap1 AB026490 Mus muscu 149723 Human gene 149723 Sequence 6 Y00508 H. sapiens BC007740 Homo sapi BC022994 Homo sapi U48963 Clarkia bere M13918 Homo sapien AX280889 Sequence AF385587 Homo sapi AF498915 Homo sapi AY065661 Gallus Description Human gene

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Hiroyasu,I., Yoshinobu,H., Marijio,P., Joel,R. and
Protein having cell calcifying inhibitory activity
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Iwamoto,M., Higuchi,Y., Yeh,H. and Pacifici,M.
Direct Submission
Submitted (05-DEC-2001) Oral Anatomy and Developmental Biology,
Osaka University Faculty of Dentistry, 1-8 Yamadaoka, Suita, Osaka
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The role of ERG (ets related gene) in cartilage development
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Transcription factor ERG variants and functional diversification of chondrocytes during limb long bone development
J. Cell Biol. 150 (1), 27-40 (2000)
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PC C12R15/09,A61K48/00,C07K14/465,C07K16/18,C12Q1/68//
PC C12R21/02,
PC C12R21/08,C12N15/00,A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT SOURCE , Organism-'Unidentified'.
                                                                                                                                                                Submitted (13-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:7143451. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                  Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: sequence_submissions@genome.wi.mit.edu
                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5471 5570: gap of 100 bp in length 7155 contig of 1585 bp in length 7156 gap of 100 bp in length 7256 gap of 100 bp 9506: contig of 2251 bp in length 9507 9606: gap of 100 bp 11993: contig of 2387 bp in length 11994 12093: gap of 100 bp in length 12094 14691: contig of 2598 bp in length 14692 14791: gap of 100 bp 17205 17304: gap of 100 bp 17305 1938: contig of 2413 bp in length 17205 17304: gap of 100 bp 19238: gap of 100 bp 21611 21710: gap of 100 bp 21611 24767: contig of 372 bp in length 26868 34107: contig of 7240 bp in length 34208 42405: contig of 7240 bp in length 42406 42505: contig of 8198 bp in length 42406 42505: contig of 8198 bp in length 42406 42505: contig of 8198 bp in length
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------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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Quality coverage: 4.1 in Q20 bases;
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          /clone_lib="RPCI-11 Human Male BAC"
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                                             /clone="RP11-32702"
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/db_xref="taxon:9606"
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                                                                                     'chromosome="11"
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143831: contig of 19209
13931: gap of 100 bp
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-351124
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RS Birren, B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faror, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Graham, L., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancarares, R., Landers, T., Lehoczk, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., Mafor, J., Maylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schauer, S., Subramanlan, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trijilio, J., Ve, W.J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Changel,Y., Collins,S., Collymore,A., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cook,A., Cooke,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Galagan,J., Gardyna,S., Changel,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.
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/rpt_family="MIR"
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/rpt_family="MLT1K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="L1ME2" 5217. .5329
                                                                                                                                                                                                                              /rpt_family="MER2"
complement/on.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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/rpt_family="(TA)n"
                                 rpt_family="L1MA9"
                                                                                                                                                                                                                                                                              /rpt_family="Tigger3b"
                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-351I24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="AluSg/x"
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REFERENCE
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KEYWORDS
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AC118263
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DEFINITION
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Brown,A., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                            Eukaryota; Metazoa; Chordata; Cra
Mammalla; Eutheria; Rodentia; Sci
1 (bases 1 to 71291)
Birren,B., Linton,L., Nusbaum,C.
Manageria,B., Clone RP24-502N12
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                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                          AC118263 71291 bp Mus musculus clone RP24-502N12,
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complement(33103. 13109)
/note="<30 qual SNGL region"
complement(33142. 13148)
/note="<30 qual SNGL region"
complement(13836. 13840)
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18764.
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/note="<30 qual SNGL region"
complement(13053. .13057)
/note="<30 qual SNGL region"
complement(13093. .13099)
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/rpt_family="L2"
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/note="<30 qual SNGL
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12876. .1307
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_family="L1MA9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-APR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into
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Center clone name: 502_N_12
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15 9644: gap of 100 bp

15 10378: contig of 734 bp

10 10478: gap of 100 bp

11 1171: contig of 693 bp

12 11271: gap of 100 bp

12 11279: contig of 708 bp
                                                                                                                                                                                                          9 8818: gap of 100
9 9544: contin ~ 5
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2302:
<sub>7ap</sub>
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5510:
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2402: gap of 100 bp
3105: contig of 652 ap
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458: gap or
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24960: contig of 7
3060: gap of 10
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19293: contig of 7
19393: gap of 10
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21700: contig of :
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42041: c
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118: gap of 100 bp

38832: contig of 714 bp

32: gap of 100 bp
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22505: contig of 705 bp
605: gap of 100 bp
23327: contig of 722 bp
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55856: contig of 722 b
5956: gap of 100 bp
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49363: contig of 707 bp 1
9463: gap of 100 bp
50136: contig of 673 bp i
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12861: contig
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                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
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Euteleostomi;
Murinae;

Foster, P.

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Hollins, B., Howells, S., Hladdun, S.L., Hodgson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Joltvet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Wa, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Martinez, B.,
Mandiney, S., Mcleod, M., Mcneill, T., Meenen, E., Milosavljevic, A.,
Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Mariney, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwookelemeh, O., Okvuonu, G.,
Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A.,
Popovic, D., Primus, E., Pu, L., L., Puazo, M., Quiroz, J., Rachlin, E.,
Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S.,
Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A.,
Sisson, I., Sitter, C., D., Smajs, D., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Sulter, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J.,
Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J.,
Wand, J., Yoon, L., Yoon, L., Yoon, V., Yu, P., Zhang, S., Wang, S., Warren, J.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Shou, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Shou, J., Shou, J.,
Shou, J., Shou, J., Steinle, M., Shou, J., Shou, J., Shou, J.,
Shou, J., Shou, J., Shou, J., Shou, J., Shou, J.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished 2 (bases 1 to 90821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,
                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                               as soon as it is available and the be preserved.
                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 42767 bases at least Q30
Consensus quality: 46297 bases at least Q30
Consensus quality: 48467 bases at least Q30
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                                                                            preserved.
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 1014: contig of 1014 bp in length 1114: gap of unknown length 2674: contig of 1560 bp in length 2774: gap of unknown length 4461: contig of 1687 bp in length
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Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Errander, P., Frantz, P., Frantz, P., Frantz, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggy, N., Ford, J., Coster, P., Frantz, P., Fantz, P., Gabisi, A., Gao, J., Garrer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunarathe, P., Hale, S., Hamilton, K., Hartins, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., King, L., Korvah, J., Kovar, C., Luz, K., Lucier, R., Luna, R., Maj, J., Louasey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus clone CH230-489C21, ***
***, 62 unordered pieces.
AC120052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently
consists of 62 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 79824 bases at least Q40
Consensus quality: 87081 bases at least Q30
Consensus quality: 91417 bases at least Q20
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Center clone name: CH230-489C21
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Harnandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Wohabbat, K., Morgan, M., Morris, S.,
Moser, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Parimus, E., Pujt, L., Ouiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GHXN
Center clone name: CH230-49G13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K.P., Brooks, S., Blakesley, R.W., Bouffard, G.G., Breen, C., Haghighi, P., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.Q., Legaspi, R., Maduro, O.L., Maduro, V.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Carnivora; Fissipedia; Felidae;
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                          Center clone name: 340I11

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 145202 bases at least Q40
Consensus quality: 145456 bases at least Q30
Consensus quality: 145735 bases at least Q20
Insert size: 130000; agarose-fp
Ouality coverage: 11.81x in Q20 bases; agarose-fp
Ouality coverage: 10.47x in Q20 bases; sum-of-contis
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Contact: nisc_mouse@nhgri.nih.gov
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., BoguslavKi, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Calangelo, M., Collins, S., Collymore, A., Cook, R., Cooke, P., Dazrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Grereira, P., FitzHugh, W., Gaye, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
                                                                                                                                                                                                                                                                               Birren,B., Nusbaum,C. and Land
Mus musculus, clone RP24-380G7
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/organism="Felis catus"
/db_xref="taxon:9685"
/clone="RP86-340111"
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3019: gap of unknown length
10407: contig of 7388 bp in length
10507: gap of unknown length
26429: contig of 15922 bp in length
26529: gap of unknown length
40137: contig of 13608 bp in length
40237: gap of unknown length
147016: contig of 106779 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.4%; Score 17; DB
100.0%; Pred. No. 74
tive 0; Mismatches
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74;
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CE, 24 unordered
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REFERENCE

JOURNAL

AUTHORS

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Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Illev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barna, N., Bastleu, v., Chazaro, B., Choepel, r., Chazaro, Camarata, J., Chang, J., Chazaro, B., Dewar, K., Diaz, J.S., Dodg Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J., Farro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Farro, S., Ferreira, P., FitzGerald, M., Grand-Pierre, N., Hagos, B., Cord.S., Graham, L., Grand-Pierre, N., Hagos, B., Cord.S., Graham, L., Grand-Pierre, N., Kamat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 21, 2002 this sequence version replaced gi:17060812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biren, B., Nusbuam, C., ------.
Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter,
Barnata. J.. Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 155816)
Birren,B., Nusbaum,C., Lander,E., Ali,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Trayers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Meneus,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Raymond,C., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 149015 bases at least Q40 Consensus quality: 152019 bases at least Q30 Consensus quality: 152932 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L1931 Center clone name: 380_G_7
                                                                                                                                                                                                                                                                                                                 Quality coverage: 6.4 in Q20 bases; agarose-fp Quality coverage: 6.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                             Insert size: 144000; agarose-fp
Insert size: 153516; sum-of-contigs
                                                                                                                                     soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
586 685; gap of 100 bp
686 1521: contig of 836 bp in length
1522 1621: gap of 100 bp
1622 2782: contig of 1161 bp in length
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  bp in length
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                                         /note="assembly_fragment" 24007. .28650
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1622. .
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/clone="RP24-380G7"
  /note="assembly_fragment"
28751. .35255
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14537: contig of 2533 l
14637: gap of 100 bp
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52189: contig of 6252 bp 1
2289: gap of 100 bp 1
57622: contig of 5333 bp 1
7722: gap of 100 bp 64527: contig of 6805 bp 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03309: gap of 100 bp
121316: contig of 18007 k
21416: gap of 100 bp
155816: contig of 34400 k
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17859: contig of 3222 l
7959: gap of 100 bp
20609: contig of 2650 l
0709: gap of 100 bp
23906: contig of 3197 l
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80807: contig of 8781 bp i
107: gap of 100 bp
91609: contig of 10702 bp
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33: gap of 100 bp
11904: contig of 2941 bp
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6539:
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45837: contig of 5947 k
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4183:
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Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Ngu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-JUL-2002) Human Genome Sequencing Center, Depa. of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced qi:20143512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (06-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center clone name: CH230-248E3
---- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: project Information
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Consensus quality: 111480 bases at least Q40
Consensus quality: 117613 bases at least Q30
Consensus quality: 122299 bases at least Q20
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Landry, C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Forder, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Forder, P., Frantz, P.,
Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Hernandez, O., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, M., J.,
Karlsson, E., Kelly, S., Khan, U., King, L., Kung, R., Ma, J.,
Lozado, R. J., Lucier, R., Lucier, R., Luna, R., Ma, J.,
Lozado, R. J., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martinez, E.,
Mansey, E., Martin, R., Martin, R., Martinez, E.,
Massey, 
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Uyun, T., Perez, L., Nguyen, N., Nickerson, E., Pace, A., Payton, B., Peery, J., Perez, L., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Puiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Police, M., Ren, Y., Peters, L., Police, R., Peters, L., Police, R., Payton, Peters, L., Payton, Peters, Peters, Payton, Peters, Peters, Payton, Peters, Pe
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Norway rat.
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
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171111 bp D.
Rattus norvegicus clone CH230-62L13,
***, 63 unordered pieces.
ACU99452
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Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this servers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scherer,S., Scott,G., Shen,H., Shooshtarl,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wieczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                         Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, X.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Licher, A., Lucler, S., Joul, W., Louiseged, H.,
Lozado, R. J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Peters, L., Pickens, R., Primus, B., Pu, L.L., Quiles, M., Ren, Y.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Terford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O.,
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Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny,D.M., Adams,C., Adio-Oduola,B., All-Osmau,r.s., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bonck, J., Bonvia & Delevia Bonck, J., Bonck, J., Bonvia & Delevia Bonck, J., Bon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Jul 11, 2002 this sequence version replaced gi:19698586
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Direct Submission
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127648 bases at least Q40
Consensus quality: 134343 bases at least Q30
Consensus quality: 138969 bases at least Q20
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17; Conservative
NOTE: This is a 'working draft' sequence. It currently consists 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 192095)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo. sapiens 192,095 genomic DNA of 11q
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Homo sapiens chromosome 11 clone RP11-660K15 map 11q, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in DataBase (2000)
2 (bases 1 to 192095)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Homo sapiens DNA, clone:RP11-660K15.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 180110 bases at least Q40 Consensus quality: 186278 bases at least Q30 Consensus quality: 189098 bases at least Q20 Insert size: 190595; sum-of-contigs Quality coverage: 5.13x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                  Center project name: HumDraftl:
Center clone name: RP11-660K15
                                                                                                                                                                                                                                                                                                                             Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                         Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
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71910 72009: gap of
72010 92865: contig of 20856 bp in length
92866 92965: gap of
92966 113193: contig of 2028 bp in length
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113294 128943: contig of 15650 bp in length
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188740 188839:
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188840
189146
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43930 44029; gap of 100 bp
44030 71909; contig of 27880 bp in length
71910 72009; gap of 100 bp
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113294. .128943
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92966. .113193
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144382. .153828
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72010. .92865
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163007. .171018
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129044. .144281
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/db_xref="taxon:9606"
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188739 contig of
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189045 contig of
190581 contig of
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189045: contig of 206 bp in length
9145: gap of 100 bp
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153828: contig of 9447 bp in length
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                                        Cooke, P.,
                                                            Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
                                                                                                                                                                                                                              Submitted (09-MAR-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195434)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-660K15
                                                                                                                                                                                                                                                                                                            Direct Submission
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188840. .189045
   DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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184488. .188739
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176065. .181418
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181519. .18438
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# ALIGNMENTS

FEATURES SOUICE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 BQ233264 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13279 row: h column: 07 High quality sequence stop: 608. Location/Qualifiers 1. 880	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 880)  1 (bases 1 to 880)  NIH-MGC http://mgc.nci.nih.gov/.  National Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished (1999)  Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov	BQ233264 880 bp mRNA linear EST 02-MAY-2002 AGENCOURT_7565836 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6041526 5', mRNA sequence. BQ233264 BQ233264 BQ233264.1 GI:20414664 EST. human. Homo sapiens

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/db_xref="taxon:9606"
/clone="IMAGE:6041526"
/clone_lib="NIH_MGC_92"
/tlssue_type="embryonal carcinoma, cell line"
/tlssue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 715)
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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/tissue_type="embryonal carcinoma, cell line"
/tab_host="DH10B (phage-resistant)" cell line"
/hab_host="DH10B (phage-resistant)" cell line"
/note="Organ; testis; Vector: pCMV-SPORT6; Site_1: NotI;
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/db_xref="taxon:9606"
/clone="IMAGE:4521233"
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CATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACGCCGAG
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Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi In
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BI713036
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Other_ESTs: ie01d08.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 473.
Location/Qualifiers
                                                                         Conservative
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                                                                                                                                                                 /note-"Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhOI; CDNA made by Oligo-dT priming. Size-selected on agarose gel. Average insert size ~Ikb. 5' XhOI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-562-1916, Pax: 314-747-2692."

a 171 c 163 g 129 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5085758"
/clone_lib="HR85 islet"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Primates;
                                                                       Score 475.4; DB 13;
Pred. No. 9.7e-136;
0; Mismatches 102;
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AU136709
Email: genomics@hri.co.jp
HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                       Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                 Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                                           HRI human cDNA project
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1 (bases 1 to 701)
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Primates;
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Nagai,T., Su
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AGENCOURT_7571287 NIH_MGC_92
5', mRNA sequence.
BQ212127
BQ212127 GI:20392058
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1089)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                        Homo sapiens
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/db_xref="taxon:9666"
/clone="PLACE1004911"
/clone_1tb="PLACE1"
/tissue_type="PLACE1"
/note="Vector: pME18SFL3"
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Contact: Robert Strausberg, Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13307 row: b column: 09
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Location/Qualifiers
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/clone=lib="NIH_MGC_92"
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally; oligo-dT pri
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technolo
Note: this is a NIH_MGC Library."
2 a 314 c 257 g 225 t 1 others
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                                                                                                                                                                               TCACGCCGAGCTATAACGCAGATATCCTCCTGTCACACCTACACTACCTCAGAGAGA---
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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University of Delaware
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illarity 87.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cogburn@udel.edu, www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle plate 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Epiphyseal Growth Plate cDNA library (pgm2n)/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Commercial broiler and Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

164 c 138 g 140 t
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//lab_host="Execution County of the C
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plate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 462; DB 13;
Pred. No. 1.4e-131;
0; Mismatches 0;
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RIKEN integrated sequence analysis (RISA) system -- 384 - format

leear EST 26-OCT-2001 smbryo lung Mus ce.  Fridae; Euteleostomi; rridae; Murinae; Mus. Hanagaki,T., Hara,A. i,J., Konno,H., Kouda a,K., Ohno,M., Tanaka,T., Toya,T., Tanaka,T., Toya,T., Tanaka,T., Toya,T., Sabe,Y., Suzuki,H., Tanaka,T., Toya,T., Sabe,Y., Suzuki,H., Sabe,Y., Suzuki,H., Tanaka,T., Toya,T., Sabe,Y., Sabata,K., Itoh yashizaki,Y., selected cDNAs to ilscovery of new awa,M., Ohara,E., Tanaka,T., Matsuura	BB660034 RIKEN full-length enriched, 13 days e musculus cDNA clone D430027L04 5', mRNA sequen BB660034 I GI:16493855 EST. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Rodentia; Sciurognathi; Nu 1 (bases 1 to 668) Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawa, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomur Okazaki, Y., Okido, T., Saito, R., Sakai, C., Saka, D., Shibata, K., Shinagawa, A., Takahashi, F., Takeda, Y., Muramatsu, M. and Hayashizaki, Y. Muramatsu, M. and Hayashizaki Laboratory for Genome Exploration Research Grostences Center(GSC), Yokobama Institute The Institute of Physical and Chemical Research 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kana Tel: 81-45-503-9216 Email: genome resegsc.riken.go.jp, Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, M., Konno, H., Okazaki, Y., Muramatsu, M. and Ha Normalization and subtraction of cap-trapper-prepare full-length cDNA libraries for rapid d genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Iz Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, Y., Ix Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K.,	SULT 7 6660034 6CESON FINITION RSION RSION GESSION GESSION ORGANISM ORGANISM ORGANISM ORGANISM ORGANISM ORGANISM ORGANISM ORGANISM
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CAAGCGAGGAGATCAG 756	AAGCAACGCAAAGAATAACAACAAGGCCAGATTTACCTTATGAGCAAGGCAGGGAGGAGGAGGCAAGGCAAGGCAAGGCAAGGCAAGGAGAGAGAGAGAAGA	697 361 757 421 817
CAGAGAGACTC 240	TCACGCCGAGCTATAACGCAGATATCCTCCTGTCACACCTACACTACCTCAGAGAGACTC  CTCTTCCACATTTGACTTCAGATGATGTTGATAAGGCCTTACAAAACTCTCCACGGTTAA GAGGAGCCACTTTATTTTTCCAAATACATCAGTTTACCCAG	181 655 241 655
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TGATGACTGCAGCGTGGCAAAAGGAGGGAAAATGGTTAGCAGTTCAGACAATGTTGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki,Y.
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTATTATTATCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I a 161 c 175 g 146 t 2 others
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/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="D430027L04"
/clone_lib="RIKEN full-length enriched, 13 days embryo
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/db_xref="taxon:10090"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, 1
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1045)
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                                                                                              GI:18505873
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Pred. No. 5.5e-126;
); Mismatches 103;
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Homo
                                  Craniata; Vertebrata; Catarrhini; Hominidae;
 Mammalian
                                                                                                                              sapiens
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NAGE:5583753
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Best Local
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                                                                 ATCCTCCTGTCACACCTACACTACCTCAGAGAGAGAGGAGCCACTTTTATTTTTCCAAAT
                                                                                                          GAACTGTGCAAGATGACCAAGGACGACTTCCAGAGGCTCACCCCCAGCTACAACGCCGAC
                                                                                                                                          GAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACGCCGAGCTATAACGCAGAT
                                                                                                                                                                           GTGAAAGAATATGGCCTTCCAGACGTCAACATCTTGTTATTCCAGAACATCGATGGGAAG
                                                                                                                                                                                                                                         GTGCCAGCAGATCCTACGTTATGGAGCACAGACCATGTACGGCAGTGGCTGGAGTGGGCA
                                                                                                                                                                                                                                                                                                                         TACATGGAAGAGCATATTCCGCCTCCAAATATGACAACCAATGAACGAAGAGTTATT 440
                                                                                                                                                                                                                                                                                                                                                                                       GTGGCAAAAGGAGGGAAAATGGTTAGCAGTTCAGACAATGTTGGGATGAACTATGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGAATTCACCTGATGACTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAGCCCGCGCGTTCCCCAGCAGGACTGGTTATCACAGCCCCCGGCCAGAGTTACCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCTTGCAAAGACAGAAATGACAGCCTCCTCTTCCAGTGAATATAGGGCAAACATCAAAG
                                              ATCCTTCTCTCACATCTTCACTACCTCAGAGAGACTCCTCTTCCACATTTGACTCCAGAT
                                                                                                                                                                                                                                                                                                        GTGGCCAAAGGCGGGAAGATGGTGGGCAGCCCAGACACCGTTGGGATGAACTACGGCAGC
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http://image.llnl.gov
plate: LLAM12347 row: f column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: (
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Organism="Homo sapiens"
/Ob_xref="taxon:9606"
/Clone="IMAGE:5583753"
/Clone=!bl="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="bH10B (phage-resistant)"
/nab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORR6; Site_1: NotI.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
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290 c 230 g 225 t
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1650 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
s., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Plunc. Genomics 2 pre, 172-186 (2001)
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, Hramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kou, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasa, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                      Please visit our web
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A630068021"
/clone_lib="RIKEN full-1
                                                                                                                                                                                                                           Location/Qualifiers
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full-length
    enriched,
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CTACAATGCCGACATTCTTCTCA
                                   CTATAACGCAGATATCCTCCTGTCA 632
                                                                            TATCGATGGGAAGGAGCTGTGCAAGATGACAAAGGATGACTTCCAGCCGCCTCACGCCGAG
                                                                                                               CATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACGCCGAG
                                                                                                                                                      GCTGGAGTGGGCGGTGAAAGAATATGGCCTCCTCGATGTGGACGTCTTACTATTTCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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/lab_host="DH10B"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japar
Tel: 81-45-503-9212
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itol.,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with tuman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                    mouse tissues
                                                                                                  oblongata"
                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6330501C04"
/tissue_type="medulla oblongata'
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                             CTATAACGCAGATATCCTCCTGTC 631
                                                                                                                                                              CATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                       TGATGACTGCAGCGTGGCAAAAGGAGGGAAAATGGTTAGCAGTTCAGACAATGTTGGGAT
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                                                                               CTACAATGCCGACATTCTTCTCTC
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Pred. No. 1.8e-122;
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                                                                                              TTAAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGAATTCACCTGATGACTGCA 318
                                                                                                                                                                           AGATGAGCCCGCGCGTTCCCCAGCAGGACTGGTTATCACAGCCCCCGGCCAGAGTTACCA 258
                                                                                                                                                                                                                                   CACACCTGGCTAAGACAGAGATGACCGCGTCCTCCTCCAGCGACTATGGACAGACTTCCA 139
                                                                                                                                                                                                                                                                       CCCACCTTGCAAAGACAGAAATGACAGCCTCCTCTTCCAGTGAATATGGGCAAACATCAA 198
GTGTGGCCAAAGGCGGGAAGATGGTGGGCAGCCCAGACACCGTTGGGATGAACTACGGCA
                                                                         TCAAAATGGAATGTAACCCTAGCCAGGTGAATGGCTCAAGGAACTCTCCTGATGAATGCA
                                                                                                                                                     Diaś Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QV4-FT0005-110500-201-f02 FT0005
AW948986
AW948986.1 GI:8126760
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson, A.J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inote="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FT0005"
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Pred. No. 2.7e-121;
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BM088063.1
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COW.
                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
BACKWARD: TOWN D COLUMN: 21
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                           WSDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                             Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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Similarity
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                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="CMV SPORT6; Site_1: NotI; Sit
                                               Library made from pooled tissue from semitendonosus muscle, longissimus adrenal, and endometrium."

177 c 159 g 104 t
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Contact: Buerstedde JM
Cellular Immunology
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/cell_type="bursa1 lymphocyte"
/dev_stage="2-3 weeks old"
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Search completed: November 9, 2002, 12:27:48 Job time: 3075.84 secs

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Maximum DB seq length: 200000000
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Copyright (c) 1993 - 2002 Compugen Ltd
                                         /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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and d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

## SUMMARIES

Result	Υ <del>[</del> [	Score	% Query Match	Length	DB	ID	Description
0	٢	387	26.7	567	10	US-09-864-761-18410	Sequence 18410, A
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	ω	276.6	19.1	549	10	US-09-923-779-54	
O	4	255	17.6	420	10	US-09-864-761-3705	
O	u	255	17.6	454	10	US-09-864-761-1653	1653,
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C	7	167.8		553	10	US-09-864-761-7427	Sequence 7427, Ap
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ი	9	163.2	11.3	477	10	US-09-864-761-5035	Sequence 5035, Ap
	Ī	163.2	11.3	519	10	US-09-864-761-12798	Sequence 12798, A
c,	•	162.2	11.2	225	10	US-09-864-761-21761	Sequence 21761, A
۵		122.4		165	10	US-09-864-761-23294	Sequence 23294, A
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ب	_	115.8	8.0	3178	9	US-10-108-605-124	124, Ap
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Sequence 101, App Sequence 563, App Sequence 3420, Ap Sequence 192, App		Sequence 309, App Sequence 320, App Sequence 12, Appl Sequence 11873, A	Sequence 23, App Sequence 3316, Ap Sequence 1788, Ap Sequence 111, App Sequence 10126, A Sequence 27055, A Sequence 23, App Sequence 24, App1 Sequence 44, App1

## ALIGNMENTS

US-09-864-761-18410/c ; Sequence 18410, Application US/09864761 ; Patent No. US20020048763A1 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04 GENERAL INFORMATION: PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. PRIOR APPLICATION NUMBER: PCT/US01/00668 PRIOR FILING DATE: 2001-01-30 FILE REFERENCE: Aeomica-X-1 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30 APPLICATION FILING DATE: FILING DATE: NUMBER: PCT/US01/00662 NUMBER: NUMBER: PCT/US01/00661 2001-01-30 2001-01-30 David K.

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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR RELING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine
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                   GCCAGCTGCTCATATGCCTTCCCCATCTTGGCACCTACTACTAA 1418
                                                                     GAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCGTGACATCTTCCAGTTTTTT
                                                                                                                                                                      GAAGATGAACTITGTAGCTCCCCATCCCCCTGCTTTTGCCCGTAACCTCATCCAGCTTTTT 1315
                                                                                                                                                                                                                          ATCTCTGTACAAGTACCCCTCAGACCTCCCGTACATGGGCTCCTATCACGCCCACCACA
                                                                                                                                                                                                                                                                                                      AGTGGCTCGGCGTTGGGGAGAGAGAGAAAAGCAAACCTAACATGAACTATGACAAACTCAG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCAACTGCATCACCTGGGAGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGA 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
CCCCACCAGCCATATGCCTTCTCATCTGGGCACTTACTACTAA
                                                                                                                                                                                                                                                                                                                                           TGCCTACAAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCCTCACCCTCCAGAATC 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGGCCCGGCGCTGGGGAGAGCGGAAGAGCCAAACCCAACATGAACTACGATAAGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCCTGGAGCTCCTGTCGGACAGCTCCAA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                  ATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACACCCCCA 1255
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ESSED IN PLACENTA, SIGNAL = 2.4

ESSED IN HEL100, SIGNAL = 1.7

ESSED IN HELA, SIGNAL = 1.7

ESSED IN HEART, SIGNAL = 0.92

ESSED IN HEART, SIGNAL = 1.8

ESSED IN LUNG, SIGNAL = 1.8

ESSED IN BRAIN, SIGNAL = 1.5

ESSED IN BRAIN, SIGNAL = 1.5

ESSED IN ADULT LIVER, SIGNAL = 1.5

ESSED IN BT474, SIGNAL = 1.5

ESSED IN BT474, SIGNAL = 0.95

ESSED IN ETTAL LIVER, SIGNAL = 0.95

ENCOT HIT: P11308, EVALUE 0.00e+00

IT: M17254.1, EVALUE 0.00e+00
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hes 85;
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Query Match Best Local S Matches 399

Similarity

24.5%; ilarity 84.4%; Conservative

Score 354.6; DB 10 Pred. No. 2.7e-104; 0; Mismatches 74;

DB 10;

Length 473;

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OTHER INFORMATION: E.
OTHER INFORMATION: N.
US-09-864-761-20472
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CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NO SOFTWARE: Annomax SEQ ID NO 20472 LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20472, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: HOMO :
FEATURE:
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron APPLICANT: Rank, David F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
FILING DATE: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00662
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                                     NN: MAP TO AP000021.2

NN: EXPRESSED IN BT474, SIGNAL = 1.2

NN: EXPRESSED IN DULT LIVER, SIGNAL = 1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1

NN: EXPRESSED IN BANIM, SIGNAL = 1.1

NN: EXPRESSED IN BORM MARKOW, SIGNAL = 0.97

NN: EXPRESSED IN PLACEWTA, SIGNAL = 1.5

NN: EXPRESSED IN HEATT, SIGNAL = 1.4

NN: EXPRESSED IN HEATT, SIGNAL
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David K.
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- US 09/608,408
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; NAME/KEY: misc_feature
; LOCATION: 356, 363, 417, 433, 442;
; LOCATION: 537, 545
; OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Eyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC
FILE REFERENCE: 210121.553
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application UP Patent No. US20020076721A1
                                                                                                                                             Matches
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          FEATURE:
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hes 332;
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                            CTCAGCCGCGCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCATGGGAAG
                                         CTCAGCCGTGCACTTCGCTACTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAA 1130
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                                                                                                                                            Conservative
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                                                                                                                                          Score 276.6; DB 10;
Pred. No. 4.6e-79;
0; Mismatches 76;
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                                                                                                                                                                      DB 10; Length 549;
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
FILE REFERENCE: Acomica-X-1
                PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                          PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,
PRIOR FILING DATE: 2000-06-30
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CURRENT FILING DATE: 2001-05-23
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  SOFTWARE:
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PRIOR APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                             APPLICATION NUMBER:
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US-09-864-761-1653/c
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR ADDITERMALE: 2001-05-23
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FEATURE:
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IOR APPLICATION NUMBER: US 60/180,312
IOR FILING DATE: 2000-02-04
IOR APPLICATION NUMBER: US 60/207,456
IOR APPLICATION NUMBER: US 09/632,366
IOR APPLICATION NUMBER: US 09/632,366
IOR FILING DATE: 2000-08-03
IOR APPLICATION NUMBER: GB 24263.6
IOR APPLICATION NUMBER: US 60/236,359
IOR APPLICATION NUMBER: PCT/US01/00666
IOR FILING DATE: 2000-09-27
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00664
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ER INFORMATION: EXPRESSED I
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ESSED IN BT474, SIGNAL = 1.2
ESSED IN ADULT LIVER, SIGNAL = 1
ESSED IN FETAL LIVER, SIGNAL = 1
ESSED IN BRAIN, SIGNAL = 1.1
ESSED IN BONE MARROW, SIGNAL = 0.97
ESSED IN PLACENTA, SIGNAL = 1.5
ESSED IN HBLLOO, SIGNAL = 1.4
ESSED IN HEART, SIGNAL = 1.4
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Pred. No. 3.5e-72;
0; Mismatches 65;
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OTHER INFORMATION: EXPRESSED IN

OTHER INFORMATION: EXPRESSED IN
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Best Local Similarity
Matches 294; Conserv
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SEQ ID NO 1653
LENGTH: 454
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ORGANISM: Homo
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FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER:
FILING DATE: 2001-01
                    ACCCCAATACCAGGCTGCCAGCTGCTCATATGCCTTCCCATCTTGGCACCTACTACTAA 1418
                                                                                                                                                                                                                                                                               ACTATGACAAACTCAGCCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAG 1119
                                                                                    CCTCATCCAGCTTTTTTGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCT
                                                                                                                                                                                                                                     CTCACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCT
 ACCCCAACATAGGCTCCCCACCAGCCATATGCCTTCTCATCTGGGCACTTACTACTAA
                                                                   CATCTTCCAGTTTTTTTGCTGCCCCCAAACCCATACTGGAATTCACCAACTGGGGGTATAT
                                                                                                                                       ATCACGCCCACCCACAGAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCCGTGA
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WMBER: PCT/US01/00669
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IN HBLADO, SIGNAL = 1.4
IN HELART, SIGNAL = 1.7
IN HEART, SIGNAL = 0.92
IN BONE MARROW, SIGNAL = 2.1
IN LUNG, SIGNAL = 1.8
IN BRAIN, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.5
IN BT474, SIGNAL = 1
IN FETAL LIVER, SIGNAL = 0.95
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RESULT 6 US-09-850-799-1 ; Sequence 1, Ap

Application

US/09850799

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US-09-850-799-1
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: Sequence 7427, Application US/09864761

: Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180, 312 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR APPLICATION NUMBER: US 9/632,366 PRIOR APPLICATION NUMBER: GB 24263.6
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Best Local Similarity 74.0%;
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APPLICANT: Hendricks, Timothy J.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Resegents and Methods for the Screening of Compounds
FILE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-03828
CURRENT APPLICATION NUMBER: US/09/850,799
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/360,779
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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Hanzel, David K.
Chen, Wensheng
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Pred. No. 1.6e-47;
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Best Local
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo
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APPLICATION NUMBER: US
FILING DATE: 2000-09-27
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                                              AGTTACCATTAAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGAA
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                                                                                                                                                                         AACATCAAAGATGAGCCCGCGGGTTCCCCCAGCAGGACTGGTTATCACAGCCCCCGGCCAG
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GGTCACCATCAAAATGGAATGTAACCCTAGCCAGGTGAATGGCTCAAGGTA 71
                                                                                                                                  INFORMATION:
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N: EXPRESSED IN PLACENTA, SIGNAL = 2.1

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76

N: EXPRESSED IN HEART, SIGNAL = 2.1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

N: EXPRESSED IN BRAIN, SIGNAL = 2.1
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RESULT 8 US-09-864-761-29364/c

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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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LENGTH: 348
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-99-27
AMERICAN AME
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       312
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                                                                                                                                                                                            Local Similarity
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APPLICATION NUMBER: PCT/US01/00668
PTIING DATE: 2001-01
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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EXPRESSED IN BONE MARROW, SIGNAL = 0.73

EXPRESSED IN ADULT LIVER, SIGNAL = 0.52

EXPRESSED IN FETAL LIVER, SIGNAL = 0.45

EXPRESSED IN FETAL LIVER, SIGNAL = 0.55

EXPRESSED IN FETAL LIVER, SIGNAL = 0.55

SMISSPROT HIT: P11308, EVALUE 4.00e-38

NT HIT: M21535.1, EVALUE 1.00e-113

EST_HUMAN HIT: AM948986.1, EVALUE 1.00e-108
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                                                                                                                                                 Score 163.2; DB 10
Pred. No. 1.3e-42;
0; Mismatches 28;
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; OTHER INFORMATION: MAP TO APO00021.2
; OTHER INFORMATION: EXPRESSED IN HEART,
US-09-864-761-5035
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                                                                                                                             SOFTWARE: Annomax SEQ ID NO 5035
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                      NUMBER OF SEQ
                                                                                                                                                                                            PRIOR FILING DATE:
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                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                 LENGTH:
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Chen, Wensheng
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RESULT 10
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Best Local
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                         IOR APPLICATION NUMBER: GB 24263.6
IOR APPLICATION NUMBER: US 60/236,359
IOR APPLICATION NUMBER: US 60/236,359
IOR FILING DATE: 2000-09-27
IOR FILING DATE: 2001-01-30
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00664
IOR FILING DATE: 2001-01-30
IOR APPLICATION NUMBER: PCT/US01/00669
IOR APPLICATION NUMBER: PCT/US01/00669
IOR APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                          OR APPLICATION NUMBER: PCT/USO1/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00662
OR FILING DATE: 2001-01-30
OR PILING DATE: 2001-01-30
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OR PILING DATE: 2001-01-30
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                                     FILING DATE: 2000-09-21
APPLICATION NUMBER: US
FILING DATE: 2000-06-30
                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/180,312 FILING DATE: 2000-02-04 APPLICATION NUMBER: US 60/207,456
APPLICATION NUMBER: US | FILING DATE: 2001-01-29
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80; Conservative
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                                                          US 09/608,408
                   09/774,203
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Pred. No. 1.7e-42;
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; OTHER INFORMATION: M
; OTHER INFORMATION: E
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US-09-864-761-12798
                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR PRICING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PRICING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
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SEQ ID NO 12798
LENGTH: 519
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE I
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
FILE REFERENCE: Acomica-X-1
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ORGANISM: Homo
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                                                                                   APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                       APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                              APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                    APPLICATION NUMBER: PCT/US01/00663
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2001-01-30
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EXPRESSED IN BONE MARROW, SIGNAL =

EXPRESSED IN ADULT LIVER, SIGNAL =

EXPRESSED IN BRAIN, SIGNAL = 0.45

EXPRESSED IN FETAL LIVER, SIGNAL =
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Pred. No. 1.8e-42;
D; Mismatches 28
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US-09-864-761-23294/c
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23294, Application Patent No. US20020048763A1 GENERAL INFORMATION:
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Best Local
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SEQ ID NO 21761
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 179;
                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION: MAP TO APO00021.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: NT HIT: M21535.1, EVALUE 1.00e-113
OTHER INFORMATION: EST_HUMAN HIT: AW948986.1, EVALUE 1.00e-108
OTHER INFORMATION: SWISSPROT HIT: P11308, EVALUE 3.00e-37
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Hanzel, David K.
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WMBER: PCT/US01/00661
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86.5%;
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GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins an
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                              US-09-925-300-420
; Sequence 420, Application
; Patent No. US20020151681A1
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Best Local :
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OTHER INFORMATION: E
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

NN: EXPRESSED IN LUNG, SIGNAL = 1.3

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76

NN: EXPRESSED IN HEART, SIGNAL = 2.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

NN: EXPRESSED IN BRAIN, SIGNAL = 2.1

NN: EXPRESSED IN BRAIN, SIGNAL = 2.1

NN: NT HIT: 9111526262, EVALUE 3.00e-88

NN: NT HIT: 9211526263, EVALUE 3.00e-88

NN: STI-HUMAN HIT: BE245360.1, EVALUE 4.00e-88

NN: SWISSPROT HIT: 911308, EVALUE 7.00e-27
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Pred. No. 1.2e
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1.2e-29;
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SEQ ID NO 420

SOFTWARE: PatentIn Ver. 2.0

PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890

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                                                                                                                                                                             ; LENGTH: 2188
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1716, Application US/09920300A Patent No. US20020136728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1716
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Best Local Similarity
                                                                                                             Matches
                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/920,300A CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: King, APPLICANT: Meagh
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE: misc feature
LOCATION: (56)
OTHER INFORMATION: n equals a,t,g,
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TYPE: DNA
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                                                                   895 CAGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCA 954
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                                                                                                                            Local Similarity
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ACTCCAACTGCATCACCTGGGAGGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATG 1014
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                                                                                                           Conservative
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                                                                                                                            Score 122.2; DB : Pred. No. 8.6e-29;
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Pred. No. 7.7e-29;
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Search completed: November Job time: 123.599 secs

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SEQ ID NO 1716
LENGTH: 2188
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1716, Application Patent No. US20020131971A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: King, Gordon E. APPLICANT: Meagher, Madeleine Joy
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                                                             GCCGGGGCTTACGCTACTATTACGACAAGAACATCATCCACAAGACGTCGGGGAAGCGCT
                                                                                            GCCGTGCACTTCGCTACTATCACAAAAATATTATGACTAAAGTTCATGGTAAACGCT 1134
                                                                                                                             AGGTGGCCCGCCGGTGGGGAAAGAGGAAAAATAAGCCCCAAGATGAACTACGAGAAGCTGA
                                                                                                                                                           AAGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTCA 1074
                                                                                                                                                                                         GCCAGTCATTCATCAGCTGGACTGGAGACGGATGGGAGTTTAAGCTCGCCGACCCCGATG
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ACGTGTACCGCTTCGTGTGCGAC
                               ATGCCTACAAATTTGATTTCCAC 1157
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# GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein protein search, using sw model

Run on: November 9, 2002, 16:46:47; Search time 29.6136 Seconds (without alignments) 1464.080 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-902-772-2 2444 1 MASTIKEALSVVSEDQSLFE.....IYPNTRLPAAHMPSHLGTYY 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB DB seq length: 0
seq length: 2000000000

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	_	Result
424.5	429	431.5	434.5	437	437.5	438	443.5	446	447	447	448	449	451.5	454	454.5	460	461	477	524	627.5	676	1227	1375	1576	1613.5	1624.5	2298	2414.5	Score
17.4	17.6		17.8	17.9	17.9	17.9		18.2	18.3	18.3		18.4	18.5	18.6		18.8	18.9	19.5	21.4	25.7	27.7	50.2	56.3		66.0			98.8	Query Match
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274

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> 61 61

PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 PARVTIKMECNPNOVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT 120

PSYNADILLSHLHYLRER-------GATFIFPNTSYYPEA

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240

PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEA

S 밁 δ 뫄 γQ В

334 301

YDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSY

393

RLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN 333

TQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSS 273

transforming prote	TVHUEK	_	428	11.7	285	5
transcription fact	S24061	_	555	11.7	286	4
ets-related protei	A46396	N	342	12.2	298.5	ω
transcription fact	S43692	_	510	12.3	300.5	ö
ETS domain protein	A43315	N	732	12.5	305	Ξ
lin-1 protein - Ca	T33103	N	393	12.7	311	5
transcription fact	B46396	_	477	12.9	314.5	9
PE-1 protein - hum	A54308	N	250	13.0	318.5	8
transcription fact	I38893	۔	477	13.1	320.5	37
transcription fact	A45938	N	110	13.1	321	8
gene pointed prote	S33167	<u> </u>	623	13.7	336	5
transforming prote	S24300	N	211	13.8	338	4
ETS2 repressor fac	S59133	N	548	13.9	340.5	ũ
transcription fact	S28820	N	94	14.1	344.5	ະ
transcription fact	S11224	2	268	14.1	345	ï
gene pointed prote	S33168	<u>,                                     </u>	718	15.5	378	ö

## ALIGNMENTS

Transcription factor erg - chicken (Sepecies: Gallus gallus (chicken) (Species: Gallus (chicken) (Species: Gallus gallus (chicken) (Species: Gallus (
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A; MOLECULE LYPE: MINAN
A; Redidues: 1-231,256-486 <REA>
A; Cross-references: GB:M17254; NID:gl82186; PIDN:AAA52398.1; PID:gl82187
R; Reddy, E.S.P.; Rao, V.N.; Papas, T.S.
PTOC. Natl. Acad. Sci. U.S.A. 84, 6131-6135, 1987
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Title: Differences: GB:M31535; NID:gl82182; PIDN:AAA35811.1; PID:gl82185
A; Cross-references: GB:M31535; NID:gl82182; PIDN:AAA35811.1; PID:gl82185
A; Title: Differentially spliced erg-3 product functions as a transcriptional activator.
A; Reference number: I58410; MUID:94119611; PMID:8290279
A; Tatus: Dreliminary: translated from GB/EMBL/DDBJ
A; Cross-references: GB:S68130; NID:g544960; PIDN:AAB29724.1; PID:g544961
A; Cross-references: GB:S68130; NID:g544960; PIDN:AAB29724.1; PID:g544961
C; Genetics: GDB:ERG
A; Cross-references: GB:S68130; NID:g544960; PIDN:AAB29724.1; PID:g544961
A; Gene: GDB:ERG
A; Cross-references: GDB:119884; OMIM:165080
A; Gene: GDB:119
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C;Date: 31-Mar-1989 #sequence_revision 30-May-1997 #t
C;Accession: A94294; A94178; I58410; A28041; A29515
R;Rao, V.N.; Papas, T.S.; Shyam, E.; Reddy, P.
Science 237, 635-639, 1987
A;Title: erg, a human ets-related gene on chromosome
A;Reference number: A94294; MUID:87263429; PMID:32997
A;Accession: A94294
A;Molecule type: mRNA
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                                  QRITTRPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSS
                                                                                                                                     SYNADILLSHLHYLRER-----
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  QRITTRPDLPYEPPRRSAWTGHGHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSS
                                                                                                  SYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGAAFIFPNTSVYPEAT
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                  HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTYY 451
                                                                                                                                                            RLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN 333
HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHMPSHLGTYY
                                                                                         YDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPDESSMYKYPSDLPYMSSY 393
                                                                                                                                        RLANPGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN
                                                                     YDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSY
                                                                     428
                                                                                                                                        368
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transforming protein fli, long splice form - hu Alternate names: Friend leukemia integration C; Species: Homo sapiens (man) C;Date: 04-Oct-1996 #sequence\_revision 30-May-1 C;Accession: 137565; S29843; S35506; A49000; A4 R;Delattre, O.; Zucman, J.; Plougastel, B.; Desmaze, C. Nature 359, 162-165, 1992
A;Title: Gene fusion with an ETS DNA-binding domain cause, Reference number: S28257; MUID:92396239; PMID:1522903 A; Molecule type: mRNA A; Accession: I37565 ;Species: Homo sapiens (man)
;Species: Homo sapiens (man)
;Species: 04-Oct-1996 #sequence\_revision 30-May-1997 #text\_change
;Date: 04-Oct-1996 #sequence\_revision 30-May-1997 #text\_change
;Accession: I37565; S29843; S35506; A49000; A49015; I54170
;Accession: I37565; A49000; A4 Status: preliminary; translated from GB/EMBL/DDBJ protein 1; transcription factor caused γģ Τ., 03-Mar-2000 Peter, translocatio **X** : Kovar, ERGB

A; Residues: 1-452 < DEL>

A;Cross-references: EMBL:X67001; NID:g32529; PIDN:CAA47399.1; PID:g32530 R;Hromas, R; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Beck, Biochim. Biophys. Acta 1172, 155-158, 1993 A;Title: Human FLT-1 localizes to chromosome 11024 and has an aberrant trans A;Reference number: S29843; MUID:93176799; PMID:8439553 A;Accession: S29843 aberrant transcript (E) Klems 'n

A; Molecule type: mRNA A; Residues: 1-68,'V',70-129,'A',131-132,'V',134-322,'Q',324-425,427-452 A; Cross-references: EMBL: M93255; NID: g182659

A; Note: the authors translated the codon GTG for residue 69 as Glu R; Hornas, R.A.; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Beck, submitted to the EMBL Data Library, May 1993
A; Description: Human FLI-1, an ETS oncogene family member preferentially expre A; Reference number: S35506
A; Recession: S35506
A; Accession: S35506
A; Accession: S35506
A; Molecule type: mRNA
A; Residues: 1-68, 'V', 70-76, 78-129, 'A', 131-132, 'V', 134-322, 'Q', 324-425, 427-452
A; Cross references: EMBL: M3255; NID: 9182659; PIDN: AAAA58479.1; PID: 9182660 expressed [F] :

Cancer Res. 52, 5833-5837, 1992
A;Title: Structure and expression of human A;Reference number: A49000; MUID:93007976; A;Status.

F11-1 gene. PMID:1394211 F11-1

Status: preliminary

A;Molecule type: mRNA
A;Rosidues: 1-322,'Q',324-452 <PRA>
A;Residues: 1-322,'Q',324-452; NID:g257353; PIDN:AAB23637.1; PID:g257354
A;Note: sequence extracted from NCBI backbone (NCBIN:115336, NCBIP:115337)
R;Watson, D.K.; Smyth, F.E.; Thompson, D.M.; Cheng, J.Q.; Testa, J.R.; Papl
Cell Growth Differ. 3, 705-713, 1992
A;Title: The ERGB/Fil-1 gene: 1solation and characterization of a new memba; Reference number: A49015; MUID:93075640; PMID:1445800
A;Accession: A49015

J.R.; Papas,

new member

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A; Status: preliminary

A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 1-390, 'Q', 392-425, 427-452 <WAT>
A; Residues: 1-390, 'Q', 392-425, 427-452 <WAT>
A; Cross-references: GB: M98833; NID: g182188; PIDN: AAA35812.1; PID: g182189
A; Cross-references: GB: M98833; NID: g182189; N

A; Note: sequence extracted from NC: R; Baud, V.; Lipinski, M.; Rassart, Genomics 11, 223-224, 1991

Genomics 11, 223-224, 1991 A;Title: The human homolog of A;Reference number: I54170; A;Accession: I54170 of the mouse common viral integration; MUID:92112219; PMID:1765382 region, FLI1,

nucleic not shown; translated from GB/EMBL/DDBJ

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ξ, 1

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transforming protein fli - mouse
N; Alternate names: Friend leukemia integration protein 1; transcript
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-3
C; Accession: $17403
R; Ben-David, Y; Giddens, E.B.; Letwin, K.; Bernstein, A.
Genes Dev. 5, 908-918, 1991
A; Title: Erythroleukemia induction by Friend murine leukemia virus:
A; Reference number: $17403; MUID:91257578; PMID:2044959
A; Accession: $17403
A; Accession: $17403
A; Residues: 1-452 <BEN>
A; Cross-references: GB:X59421; NID:g50974; PIDN:CAA42055.1; PID:g509
A; Genetics:
A; Gene: Fii
C; Superfamily: transcription factor erg; ets DNA-binding domain home
C; Keywords: DNA binding; nucleus; proto-oncogene; transcription fact
F; 118-192/Domain: ets RII regulatory region homology <ETR>
F; 283-361/Domain: ets DNA-binding domain homology <ETR>
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A;Residues: 1-6 <BAU>
A;Cross-references: GB:L47616; NID:g1000863; PIDN:AAA76854.1; PID:g1000864
C;Genetics:
A;Gene: GDB:FLI1
A;Cross-references: GDB:127565; OMIM:193067
A;Map position: 11q24.1-11q24.3
A;Introns: 77/3
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; tr F;118-192/Domain: ets RII regulatory region homology <ETR>
F;283-361/Domain: ets DNA-binding domain homology <ETS>
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Pred. No. 1.1e-110;
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- PMRVNIKREY - - EHMNGSRESPVDCSINKCSKLIGGSEGNAMTY - TYMDEKNGPPPPNM

118

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В

61 60

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C; Geneti
A; Gene:
                                                                                                                                                         C;Superfamily: transcription factor erg; ets DNA-binding domain C;Keywords: DNA binding; nucleus; proto-oncogene; transcription F;117-191/Domain: ets RII regulatory region homology <ETR> F;284-362/Domain: ets DNA-binding domain homology <ETS>
                                                                                                                                                                                                                                                                                                    R;Meyer, D.; Wolff, C.M.; Stiegler, P.; Sen Mech. Dev. 44, 109-121, 1993
A;Title: X1-fli, the Xenopus homologue of A;Reference number: S49013; MUID:94206844;
A;Accession: S49013
                                                                                                                                                                                                                                                                                                                                                                                         transforming protein fil - African clawed frog
N;Alternate names: Friend leukemia integration prot
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 23-May-1997
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A; Residues: 1-453 <A
A; Cross-references:
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MDGTIKEALSVVSDDQSLFDSAYGASSHLSKADMTASANPDYGQPHKINPIPPQQDWINQ
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                                                                                                    52;
                                                                                                                                                                                                                                               NID:g505486;
                                                                                                                Score 1576;
Pred. No. 3
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5; Mismatches
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ches 85;
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3.6e-107;
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RESULT 6
$29844

K;Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
C;Species: Homo sapiens (man)
C;Deccies: New y, W; Denny, C.; Raskind, W; Moore, J; Maki, R.A.; Beck, E.; Klemsz, Biochim. Biophys. Acta 1172, 155-158, 1993
A;Title: Human FLI-1 localizes to chromosome 11024 and has an aberrant transcript in neu A;Reference number: $29844
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-385 <HRO>
A;Ccoss-references: EMBL:M93255; NID:g18265; PIDN:AAA58480.1; PID:g182661
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1992
C;Genetics:
A;Gene: GDB:FLI1
A;Cross-references: GDB:127565; OMIM:193067
A;Map position: 11q24.1-11q24.3
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regula C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factory region homology cETR>
F;217-295/Domain: ets DNA-binding domain homology cETS>
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EDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTD
                                                                                                                                                                                                                                   SRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNMTTNERRVIVPADPTLWST 136
                                                                                                                                           E--SSLLAYNTTSHTDQSSRLSVKEDPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKN
                                                                                                                                                                                                                EHVROWLEWAIKEYSLMEIDTSFFONMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLR
                                                                                                                                                                                                                                                                                      ARESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNMTTNERRVIVPADATLVTQ
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                                                                       TEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSANASCITWEGTNGEFKMTD
                                                                                                                                                                             ERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQ-PSSSTVPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKSIMTKVHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPVTKSPPMGGTQNVNKSGDQQRSQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPTQSKATQPSSSTVPKTED-QRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDS
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A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-173 <QDA>A; Residues: 1-173 <QDA>A; CRESIdues: 1-173 <QDA>A; CRESIdues: 1-173 <QDA: NID: 9161310; PIDN: AAA68905.1; PID: 9161311 C; Superfamily: transcription factor erg; ets DNA-binding domain homology; C; Keywords: DNA binding; nucleus; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: mRNA
A; Residues: 1-272 <RIV>
A; Cross-references: GB.566169; NID:g436276; PIDN:AAB28525.1; PID:g436277
A; Cross-references: GB.566169; NID:g436276
A; Cross-references: GB.566169; NID:g436277
A; Experimental source: pre-B-cell line 22D6
A; Note: sequence extracted from NCBI backbone (NCBIN:138523, NCBIP:138524)
A; Note: sequence extracted from NCBI backbone (NCBIN:138523, NCBIP:138524)
C; Superfamily: transcription factor erg; ets DNA-binding domain homology; ets F; 140-218/Domain: ets DNA-binding domain homology <ETS>
                                                                                                       R;Qi, S.; Chen, Z.Q.; Papas, T.S.; Lautenberger, J.A. DNA Seq. 3, 127-130, 1992
A;Title: The sea urchin erg homolog defines a highly A;Reference number: A56646; MUID:93091246; PMID:14578
A;Accession: A56646
A;Status: preliminary
                                                                                                                                                                                                                                          transcription factor erg/fli-1 homolog - sea urchin (Lytechinus variegatus) (fragment C;Specias: Lytechinus variegatus (variegated urchin) C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 16-Jul-1999 C;Accession: A56646
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A54617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE
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mes: Ig heavy chain enhancer-binding protein
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Pred. No. 4.7e-82;
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                          homology;
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A L

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A; Status: preliminary; translated f; A; Molecule type: DNA A; Residues: 1-377 <STE> A; Cross-references: EMBL: U39470; PII A; Experimental source: strain Brist(C; Genetics: A; Gene: CESP: T08H4.3 A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-179 <LEL>
C; Superfamily: transcript
C; Keywords: DNA binding;
F; 7-85/Domain: ets DNA-bi
                                                                                                                                                                                                                                  TBSULT 10
T94343
hypothetical protein T08H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t.
C;Accession: T34343
                                                                                                                                                                      R;Stellyes, L.
submitted to the EMBL Data Library, Octobe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor erg/fli-1 homolog - polychaete (Nereis diversicolor) (fragment) (;Species: Nereis diversicolor (sandworm) C;Date: 15-7ul-1995 #sequence_revision 23-May-1997 #text_change 30-May-1997 C;Accession: S51226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;6-84/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: transcription factor erg; ets DNA-binding; Reywords: DNA binding; nucleus; transcription factor; 7-85/Domain: ets DNA-binding domain homology <ETS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNFVAPHPPALPVTSSSFFAAPNPYWNSPTG-GIYPN---TRLPAAHMPSHLGTYY 451
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                                                                                                                                                                                                                                                                                                                                                                                                                  KMNFVAPHPPALPVTSSSFFAAPNPYWNSPTG-GIYPNTRLPA-----AHMPSHLGTYY 451
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                                                       EMBL:U39470; PIDN:AAC71120.1; GSPDB:GN00020; CESP:T08H4 be: strain Bristol N2; clone T08H4
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68.2%;
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Pred. No. 1.3e-38;
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Pred. No. 3.5e-42;
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A;Introns: 80/2; 104/3; 151/1; 187/3
C;Superfanily: ets DNA-binding domain homology
F;37-115/Domain: ets DNA-binding domain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-208 <HAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, April A; Description: The sequence of C. elegans A; Reference number: Z18405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Hallsworth,
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:C42D8.4
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Best Local
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STSSNQIIPPSTAT --
                              FVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAH
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                                                                 LAQACQSAILTNGGNPNGDLSSTVHSLS--PYTNQVLPIGVTSRLSTSMSSYHSILSSTS
                                                                                                                                    SNGEFKLYDPDEVARKWGERKSKPNMNYDKLSRALRYYYDKNIMTKVQGKRYAYKFDFQG
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YWSTPQSSL-TYTGMPSSY
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                                                                                                                                                                                                                                                                           Score 477; DB 2; Length 208
Pred. No. 1.4e-27;
9; Mismatches 41; Indels
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Pred. No. 1.2e-30;
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RESULT 12 A40858 GA-binding F N; Alternate

e names:

alpha (GABPA;

chain - m

mouse

respiratory

factor-2 alpha chain; transcription

fac

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A;Title: Identification of ets- and notch-related subunits in GA bin A;Reference number: A40858; MUID:91343912; PMID:1876836 A;Accession: A40858; MUID:91343912; PMID:1876836 A;Accession: A40858
A;Accession: A40858
A;Accession: A40858
A;Accession: PA54 <LAM>
A;Cross-references: GB:M74515; NID:g193382; PIDN:AAA53030.1; PID:g1:A;Accession: Pata of this sequence were determined by protein sequencing C;Genetics: A;Acene: Gabpa A;Map position: 16 47.0
C;Complex: GA-binding protein is a heterotetramer of two alpha and 10;Function: A;Pathway: known to promote transcription of apolipoprotein A-II, C;Csuperfamily: transcription factor els; ets DNA-binding domain home C;Reywords: DNA binding; nucleus; transcription factor F:174-245/Domain: ets RII regulatory region homology <ETR>
F;322-400/Domain: ets DNA-binding domain homology <ETR>
                                                                                                                                                                                                                                                                       RESULT 13
A48146
GA-binding
                                                                                    Mol. Cell. Biol. 13, 1303-1354, 2500
A;Title: cDNA cloning of transcription factor E4TF1 subunits
A;Reference number: A48146; MUID:93180783; PMID:8441384
                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 23-May-1997
C;Accession: A48146; A46303; A55903
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C;Date: 28-Feb-1992 #sequence_revision 23-May-1997 #text_change 16-Jul-1999
C;Accession: A40858
R;LaMarco, K.; Thompson, C.C.; Byers, B.P.; Walton, E.M.; McKnight, S.L.
Science 253, 789-792, 1991
                       A; Residues:
                                      A;Status: not compared with conceptual A;Molecule type: mRNA; protein
                                                                                 A; Accession: A48146
                                                                                                                                                               R; Watanabe, H.; Sawada,
                                                                                                                                                                                                                                                     N; Alternate
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  A; Note:
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Best Local
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                                                                                                                                            Cell. Biol. 13, 1385-1391, 1993
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  sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     KVHGKRYAYKF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPTTIKVINSSAKAA-----KVQRSP-RISGEDRS---SPGNRTGNNGQIQLWQFLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARR--SAWTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRSLFDQG-----VKTDGTVQLSVQVISYQGMEPKL---NILEIVKTAETVEVVIDPD- 127
                                                                                                                                                                                                                                                                                                                                                                            KVQGKRFVYKFVCDLKTLIGYSAAELNRLVIECEQKKLARMQLHGIAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLTDKDARDCISWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDGDMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPG-----SGQIQLWQFLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKEQERLGIPYDPIRWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AHHAEAEAHLVEEAQVITLDGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNER-------
                                                                                                                                                                                                                                                     protein alpha chain - human
e names: GABPA; nuclear resp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123;
                       1-454 <WAT>
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  extracted
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                                                                                                                                                                                                                                                 nuclear respiratory factor-2 alpha chain;
  from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g193382; PIDN:AAA53030.1; PID:g193383 were determined by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
NCBI backbone (NCBIP:125762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 461; DB 1;
Pred. No. 6.2e-26;
                                                                                                                                                                 K.; Yamaguchi, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                            translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVLASQEQQMNEIVTIDQPVQIIPASVPP
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                                                                                                                                                                                                        #text_change 16-Jul-1999
                                                                                                                                                                 Goto, M.;
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                                                          A; Reference number: A; Accession: S37616
                                  A; Status: preliminary
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A;Residues: A; Molecule

type: DNA : 1-464 <T 1-464

MUID:93096481;

structural organization of B1; PMID:1461651

D-elg,

an

ets

prot

T.S.;

Watson,

D.K.;

Schulz, R.A.

#text\_change

16-Jul-1999

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RESULT
S37616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ets-related protein.

A;Reference number: A55903; MUID:95001929; PMID:7918435

A;Rocession: A55903

A;Molecule type: protein
A;Residues: 26-34,'A',36,'X',38,'X',40-46;151-165;167-174;350-359

C;Genetics: C;Genetics: A;Gene: GDB:GABPA; E4TF1-60; E4TF1A
A;Gene: GDB:GABPA; E4TF1-60; E4TF1A
A;Cross-references: GDB:138476; OMIM:600609

A;Map position: 21q21-21q22.1
C;Gomplex: GA-binding protein is a heterotetramer of two alpha and C;Function:
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision :
C;Accession: S37616; S28822
R;The, S.M.; Xie, X.; Smyth, F.; Papas,
Oncogene 7, 2471-2478, 1992
A;Title: Molecular characterization and
A;Reference number: S37616; MUID:9309648
                                                                                                                                                              transcription factor elg - fruit fly (D. N;Alternate names: transcription factor
                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: a transcription factor that binds A; Pathway: known to promote transcription of apol C; Superfamily: transcription factor elg; ets DNA-C; Keywords: DNA binding; nucleus; transcription f; 174-245, Domain: ets RII regulatory region homol
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Biochemistry 33, 12139-12148, 1994
A;Title: Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Identity of GABP with NRF-2, a multisubunit activator of cytochrome oxidase A;Reference number: A46303; MUID:93194058; PMID:8383622 A;Accession: A46303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 237-248; 429-448 < VIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: parts of this sequence were determined R;Virbasius, J.V.; Virbasius, C.A.; Scarpulla, Genes Dev. 7, 380-392, 1993
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Best Local
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                                                                                                                                                                                                                                                                                                         QLHGIAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNM 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHIPPPNMTTNER-------RVIVPADPTLWSTDHVRQWLEWAVKEYGLPD 154
                                                                                                                                                                                                                                                                                                                                                                                             NYEKLSRALRYYYDGDMICKVQGKRFVYKFVCDLKTLIGYSAAELNRLVTECEQKKLAKM 429
                                                                                                                                                                                                                                                                                                                                                                                                                                          NYDKLSRALRYYYDKNIMTKVHGKRYAYKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRTGN--NGQIQLWQFLLELLTDKDARDCISWVGDEGEFKLNQPELVAQKWGQRKNKPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEQQMNEIVTIDQPVQIIPASVQSATPTTIKVIN-SSAKAAKVQ-RAPRISGEDRSSP-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRITTRPDLPYEQARR--SAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDLTTL-NISGRELCSLNQEDFFQRVP--RGEILWSHLELLRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHITTISDETSEQVTRWAAALEGYRKEQERLGIPYDPIQWSTDQVLHWVVWVMKEFSMTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109;
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35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 460; DB 1;
Pred. No. 7.3e-26;
                                                                                                                                                                                      (Drosophila
                                                                                                                                                                   ets-97D
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                                                                                                                                                                                      melanogaster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (via the alpha chain) to lipoprotein A-II, cytochro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
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A;Gene: FlyBase:Ets97D
A;Cross-references: FlyBase:FBgn0004510
A;Introns: 22/1; 60/2; 83/3; 322/1
A;Introns: 22/1; 60/2; 83/3; 322/1
C;Superfamily: transcription factor elg; ets DNA-binding domain homology; ets RII regul: C;Keywords: DNA binding; nucleus; transcription factor F;190-263/Domain: ets RII regulatory region homology <ETR>F;348-426/Domain: ets DNA-binding domain homology <ETS>
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R;Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
Dev. Biol. 151, 176-191, 1992
A;Title: Isolation and characterization of five Drosophila genes that encode an ets-rel A;Reference number: S28819; MUID:92249640; PMID:1577186
A;Accession: S28822
                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: I38739
R;Gugneja, S.; Virbasius, J.V.; Scarpulla, R.C.
Mol. Cell. Biol. 15, 102-111, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nuclear respiratory factor-2 subunit alpha - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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A;Residues: 298-449 <CHE>
A;Cross-references: EMBL:M88471; NID:g157189; PIDN:AAC34199.1; PID:g552088
A;Note: the authors translated the codon AGC for residue 302 as Thr
C;Genetics:
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                                                                                                                                                            A;Cross-references: EMBL:U13044; NID:g531892; PIDN:AAA65706.1; PID:g531893 C;Superfamily: transcription factor elg; ets DNA-binding domain homology; ets RII regula F;174-245/Domain: ets RII regulatory region homology <ETTR> F;322-400/Domain: ets DNA-binding domain homology <ETS>
                                                                                                                                                                                                                                                                                            A;Title: Four structurally distinct, non-DNA-binding subunits of human nuclear respirate A;Reference number: I38739; MUID:95097980; PMID:7799916 A;Accession: I38739 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-454 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMRKSYQSVKSSDSVESTTSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107;
                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                            Score 454; DB 2;
Pred. No. 2e-25;
                                                                       Mismatches
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RVIVPADPTLWSTDHVRQWLEWAVKEYGLPD 154
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                                                                    64; Indels 120;
                                                                                                                 Length 454;
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	404 KTLIGYSAAELNRLVTECEOKKLAKMOLHGIAO 436	404	В
	363DFHGIAQ 369	363	Qy
403	344 DEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDGDMICKVQGKRFVYKFVCDL 403	344	뮹
362	307 TNGEFKMTDPDEVARRWGERKSKPNWNYDKLSRALRYYYDKNIMTKVHGKRYAYKF 362	307	Qy
343	284 IKVINKCAKAAKVQRAPRISGEDRSSPGNRTGNNGQIQLWQFLLELLTDKDARDCISWVG 343	284	ф
306	273 SRLANPGSGQIQLWQFLLELLSDSSNSNCITWEG 306	273	Qy
283	255 QEQQMNEIVTIDQPVQIIPASVQSATPTT 283	255	В
272	215 QRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTS 272	215	Qy
254	210 IDLTTL-NISGRELCSLNQEDFFORVPRGEILWSHLELLRKYVLAS 254	210	Db
214	155 VDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRERGATFIFPNTSVYPEAT 214	155	Qy
209	150 KHITTISDETSEQVTRWAAALEGYRKEQERLGIPYDPIQWSTDQVLHWVVWVMKEESMTD 209	150	Ъ

Search completed: November 9, 2002, 16:54:38 Job time: 30.6136 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEW=xlp
-Q-/cgn2_1/USPTO_spool/US09902772/runat_07112002_134033_9031/app_query.fasta_1.1294
-Q-/cgn2_1/USPTO_spool/US09902772/runat_07112002_134033_9031/app_query.fasta_1.1294
-DB-GenEmb1 -QFWT_fastap -SUFFIX-rge -MINMATCH-0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09902772_GCGN_1_1_3441_@runat_07112002_134033_9031 -NCDU=6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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36: em_htg_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1 Wamoto,M., Higuchi,Y., Enomoto-Iwamoto,M., Kurisu,K., Koyama,E., Yeh,H., Rosenbloom,J. and Pacifici,M.

The role of ERG (ets related gene) in cartilage development Osteoarthr. Cartil. 9 Suppl A, S41-S47 (2001)
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Yeh,H., Abrams,W.R., Rosenbloom,J. and Pacifici.M.
Transcription factor ERG variants and functional diversification
chondrocytes during limb long bone development
J. Cell Biol. 150 (1), 27-40 (2000)
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NPGSGQIQLMQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY
DKLSRALRYYDKNILMTKVHGKRYAYKFDFHGIAQALQPHPESSMYKKYESDLPYMSS
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1236	TACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACCCCCCAGAAGATG	1177	DЬ
400	TyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisAlaHisProGlnLysMet	381	Qγ
1176	AAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCCTCACCCTCCAGAATCATCCATG	1117	В
380	LysPheAspPheHisGlyIleAlaGlnAlaLeuGlnProHisProProGluSerSerMet	361	ΩУ
360 1116	LeuArgTyrTyrTxyrAspLysAsnIleMetThrLysValHisGlyLysArgTyrAlaTyr 	341 1057	β δ
1056	CGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTCAGCCGTGCA	997	В
340	ArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAla	321	QΥ
996	TGCATCACCTGGGAGGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGAAGTGGCT	937	日
320	CysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAla	301	Qγ
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876	CAGTTAGATCCTTATCAGATTCTTGGACCGACCAGCCGTCTTGCAAATCCAGGGAGT	817	Ъ
280	GlnLeuAspProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySer	261	VΩ
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240	ProAspLeuProTyrGluGlnAlaArgArgSerAlaTrpThrSerHisSerHisProThr	221 697	5 6
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220 .	${\tt ThrPheIlePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArg}$	201	γQ
200 636	ProSerTyrAsnAlaaspIleLeuLeuSerHisLeuHisTyrLeuArgGluArgGlyAla 	181 577	β δ
576	CAGAACATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACG	517	Db
180	GlnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThr	161	Qy
160 516	141 GlnTrpLeuGluTrpAlaVallysGluTyrGlyLeuProAspValAspIleLeuLeuPhe 160 	141 457	Qy Db
456	ANTGAACGAAGAGTTATTGTGCCAGCAGATCCTACGTTATGGAGCACAGACCATGTACGG	397	DЬ
140	AsnGluArgArgVallleValProAlaAspProThrLeuTrpSerThrAspHisValArg	121	Qy
396	GGGATGAACTATGGAAGCTACATGGAAGAGAAGCATATTCCGCCTCCAAATATGACAACC	337	Дδ
120	GlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProPsoAsnMetThrThr	101	Qy
100 336	SerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnVal	81 277	ρ 9
276	CCGCCAGAGTTACCATTAAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGAAT	217	뫄
80	ProAlaArgValThrIleLysMetCluCysAsnProAsnGlnValAsnGlySerArgAsn	61	Qy
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400 1262	TyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisAlaHisProGlnLysMet (	381 1203	Qy db	
380 1202	LysPheAspPheHisGlyIleAlaGlnAlaLeuGlnProHisProProGluSerSerMet	361 1143	Qy Db	
360 1142	LeuArgTyrTyrTyrAspLysAsnIleMetThrLysValHisGlyLysArgTyrAlaTyr 	341 1083	Qy Db	
340 1082	ArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAla	321 1023	Оу	
320 1022	CysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAla	301 963	Qy Db	
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260 842	GlnSerLysAlaThrGlnProSerSerSerThrValProLysThrGluAspGlnArgPro	241 783	Qy Db	
240 782	ProAspLeuProTyrGluGlnAlaArgArgSerAlaTrpThrSerHisSerHisProThr 	221 723	dd Vo	
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Duterque-Coquillaud,M.
Direct Submission
Submitted (17-JAN-1994) M. Duterque-Coquillaud, CNRS UA 1160,
Oncologie Moleculaire, Institut Pasteur, 1 rue Calmette, 5901
Lille, FRANCE
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Gallus gallus
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1 (bases 1 to 1516)

1 (bases 1 to 1516)

1 (bases 1 to 1516)
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Duterque-Coquillaud,M.
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58 a 392 c 327 g 339 t
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63. .1499
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AUTHORS
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OS Unidentified
PN JP 199075871-A/2
PN 199075871-A/2
PD 23-MAY-1999
PF 29-MAY-1998 JP 1998166076
PR 18-JUN-1997 US 60/050297 PI
HIROYASU IWAMOTO, YOSHINOBU HIGUCHI, MARIJIO PASHIFIKI, PI JOEL
ROZENBURCOM,
PC C12P1/09, A61K48/00,C07K14/465,C07K16/18,C12Q1/68//A61K38/0
PC C12P21/09,C12N15/00,A61K37/02
PC C12P21/08,C12N15/00,A61K37/02
CC Strandedness: Single;
PH Key Location/Qualifiers
FT source /organism='Unidentified'.
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Hiroyasu, I., Yoshinobu, H., Marijio, P., Joel, R. and Helena, E. Protein having cell calcifying inhibitory activity and gene
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                                                                                                                                          ArgLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeu
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362 120 422 140 140 482 160

602 198 662 198 100

242 80 302 40 182 60 122

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                                                                                                                                                                                                                                                                                                   (E-mail:hattori@gsc.riken.go.jp, URL:ht
Tel:81-45-503-9111, Fax:81-45-503-9170)
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Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
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148. .1608
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                                                                                                                                               /codon_start=1
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GCCTACGGAACGCCACCCTGGCTAAGACAGAGATGACCGCATCCTCTTCCAGTGACTAT
                      AlaSerThrI1eLysGluAlaLeuSerValValSerGluAspGlnSerLeuPheGluCys
{\tt ArgLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeu}
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Submitted (24-FEB-1998) P
National de la Recherche
                                                                                                                                                                                                Baltzinger,M., Mager-Heckel,A.M. and Remy,P. X1 erg: expression pattern and overexpression during plead for a role in endothelial cell differentiation Dev. Dyn. 216 (4-5), 420-433 (1999) 20099678
                                                                                                                                                                                                                                                                                                         AJ224126.1 GI:5420047
ERG gene; transcription factor.
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                       Xenopus laevis.
Xenopus laevis
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225. .1595
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225. .1595
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                                                                                                                  Location/Qualifiers
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        TyrGluGlnAlaArgArgSerAlaTrpThrSerHisSerHisProThrGlnSerLysAla
                                                                               ProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAspLeuPro
                                                                                                                                                                                                                      VallleValProAlaAspProThrLeuTrpSerThrAspHisValArgGlnTrpLeuGlu
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M17254
M17254.1 GI:182186
erg 2 protein.
Human cell line COLO 320,
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                                                                                                                       Rao, V.N., Papas, T.S. and Reddy, E.S. erg, a human ets-related gene on chromosom splicing, polyadenylation, and translation Science 237 (4815), 635-639 (1987)
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 3166)
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Percent Similarity:
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Query Match:
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509. .516
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3143. .3149
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DVNILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHILTSDDVDKA
LQNSPALMHARNTDLPYEPPRRSAWTCHGHPPPQSKAAQPSPSTVPKTBDQRPQLDPY
QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRW
GERKSKPNMNYDKLSRALRYYDKNIMTKVHGKRYAYKEDFHGIAQALQPHPPESSLY
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                2 (bases
Aoki,T., T
Komurasaki,
Direct Subm
                                                                                                                                                           specific protein
AB031088
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                vascular endothelial cell specific Rattus norvegicus liver cDNA to mRI
                                                                                                                                                 AB031088.1 GI:15128488
                                                                                                                                                                              Rattus
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                                                                        Aoki,T.,
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                                                      Identification of VESP14,a
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| norvegicus VESP14 mRNA
                 Toyoda, H.,
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Rodentia;
                                                                       Nishimoto,S.,
                 Nishimoto, S.,
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A for
                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                 Tawara, J.,
                                                                       Tawara, J.,
                                                                                                                                                                              vascular
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endothelial cell
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US-09-902-772-2 (1-451) x AB031088
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                           GlnTrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuPhe
                                                                                                                                    GlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProProAsnMetThrThr
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CAGTGGCTGGAGTGGAAAGAATACGGCCTCCTAGACGTGGACGTCTTATTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510
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/product="pascular"
/product="pascular
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63. .1430
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/tissue_type="liver"
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RESULT 9
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Eukaryota;
Mammalia; E
                                                         AB073079 2133 bg
Mus musculus Erg mRNA, mouse hc
transcript variant 2, complete
AB073079
AB073079.1 GI:16197542
                                      Mus
                              musculus
                                      musculus
         Eutheria;
                                      CDNA
                                     to mRNA,
         Chordata;
Rodentia;
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                                     clone:Erg-2
                                                                                     bp mRNA
homolog of
        Sciurognathi;
                  Craniata; Vertebrata;
                                                                                       Human
                                                                                    linear ROD 17-OCT-2001 nan ets-related gene ERG,
         Muridae;
       Euteleostomi;
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Ozawa,R., Noguchi,H.,
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WGERKSKPNMYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPESSL
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MetSerProArgValProGlnGlnAspTrpLeuSerGlnProProAlaArgValThrIle 66	CATCTTACTAAAACGGAGATGACCGCATCTTCCTCCAGTGACTATGGGCAAACCTCGAAA 485			Alignment Scores:  Pred. No.:  9.331e-141  1798  Score:  2153.50  Percent Similarity:  84.538  Query Match:  88.118  Mismatches:  29  Caps:  Gaps:  339  Caps:  349  Conservative:  21  Caps:  350  Caps:  360  Caps:  370  Caps:  Ca	/gence"erg" /function="transcription factor" /function="transcription factor" /codon_start=1 /protein_id="CAB46566.1" /protein_id="CAB46566.1" /db_xref="GI:5420046" /db_xref="SpTREMBL:Q9W700" /db_xref="SpTREMBL:Q9W700" /translation="MOHMAFIPTYEDYSNEALSVVSEDQSLFECTYGTPHLTKTEMTA	/yeine- eiy 3211778	/organism="xenopus laevis" /db_xref="taxon:8355" /clone="lambda ZAPII-erg A" /clone_lib="lambda ZAPII" /dev_stage="stage 30 embryo" 321. 1778	11798	Submitted (24-FEB-1998) Baltzinger M., UPR9005, MMDCD, Centre National de la Recherche Scientifique, 15, RUE Rene Descartes, 67084, FRANCE Location/Qualifiers		Dev. Dyn. 216 (4-5), 420-433 (1999) 20099678 10633861	1 (bases 1 to 1798)  Baltzinger, M., Mager-Heckel, A.M. and Remy, P.  XI erg: expression pattern and overexpression during development plead for a role in endothelial cell differentiation	Xenopus laevis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae: Xenopus	AJ224125.1 GI:5420045 ERG gene; transcription factor.	XLAJ4125 1798 bp mRNA linear VRT 21-JAN-2000 Xenopus laevis erg gene (erg_A). A1724125	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted (16-OCT-2001) Masahira Hattori, The Institute of Ph. and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, (E-mail:hattori@qsc.riken.go.jp, URL:http://hgp.gsc.riken.go.Tel:81-45-503-9111, Fax:81-45-503-9170)
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Ozawa, R., Noguchi, H., Taylo
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/db_xref="taxon:10090"
/chromosome="16"
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                                                                          AGCCGCCTTGCTAATCCAGGTAGTGGCCAGATCCAGCTGTGGCAGTTCCTGCTCGAACTC
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78 150	9-902-	Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB:	COUNT	CDS	sourc	JOURNAL MEDLINE PUBMED	AUTHORS TITLE	S S S S S S S S S S S S S S S S S S S	YWORDS GMENT URCE	RESULT 12 HUMERG11 LOCUS DEFINITION ACCESSION VERSION	1477	433	1417	413	1357	393	1297	373	1237	353	1177
SerArgAsnSerProAspAspCygSerValAlaLysGlyGlyLysMetValSerSerSer 97 	772-2 (1-451) x HUMERG11 (1-3126)	nment Scores:       5.6e-117       Length:       3126         1. No.:       1810.00       Matches:       336         cent Similarity:       90.34%       Conservative:       10         c Local Similarity:       87.73%       Mismatches:       23         cy Match:       74.06%       Indels:       14         cy Match:       9       Gaps:       4	//IOCe="ergl procein" /Codon_start=1 /protein_id="AAA35811.1" /protein_id="AAA35811.1" //db_xref="GI:182185" //tanslation="MyGSpdTvGMNYGSYMEEKHMPPPNMTTNERRVIVPADDTLWST /translation="WGSPDTVGMNYGSYMEEKHMPPPNMTTNERRVIVPADDTLLSHLHY /translation="WGSPDTVGMLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHY LRETFLPHLTSDDYDKALQNSPRLMHARNTDLP*EPPRRSAWTGHFPPQSKAAQPS SETYPKTEDQRQFLDPYQILGPTSSRLANPGSGQIQLWGFLLELLSDSSNSSCITWEG STYPKTEDQRFQLDPYQILGPTSSRLANPGSGQIQLWGFLLELLSDSSNSSCITWEG TNGEFKMTDDDEVARRWGERKSKINMNYKKLSRALRYYKDKNIMTKVHGRYXAYKFDF HGLAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPN PYMNSPTGGIYPNTRLPTSHMPSHLGTYY" 928 a 732 c 725 g 741 t  1 bp upstream from EcorI site.	/organism="Homo Sapiens" /db_xref="taxon:9606" 1951286		. U.S.A. 84 (17), 6131-6135 (19	o the ets oncogen		erg protein. 1 of 2 Human, cell line C	HUMERG11 3126 bp mRNA linear PRI 27-APR-1993 HUMEN erg protein (ets-related gene) mRNA, complete cds. M21535 M17390 M21535.1 GI:182182	TACCCGAACACTAGGCTCCCAGCCAGCCATATGCCCTCACCTGGCCACCTACTAC 1533	TyrProAsnThrArgLeuProAlaAlaHisMetProSerHisLeuGlyThrTyrTyr 451	ACATCTTCCAGTTTCTTTGCTTCCCCGAACCCATACTGGAATTCACCGACTGGGGGCATC 1476	ThrSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIle 432	TATCACGCCCACCCCAGAAGATGAACTTTGTGTCTCCCCACCCTCCCGCTCTCCCAGTC 1416	TyrHisAlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProVal 412	CCCACCTCCTGAGTCGTCCCTGTACAAGTACCCCTCCGACCTGCCATACATGGGCTCC 1356	ProHisProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSer 392	GTGCACGGGAAGCGCTACACCTACAAGTTTGACTTCCACGGGATTGCCCAGGCCCTGCAG 1296	ValHisGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGln 372	AACTATGACAAGCTCAGCCGCGCCCTCCGCTACTACTACGACAAAAACATCATGACCAAG 1236

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AJ249590
AJ249590.1 GI:6006476
fli-1 gene; Fli-1 proto
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Sharrocks, A.D.
Direct Submission
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Mech. Dev. 90 (2)
20108585
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ETS-domain transcription factor Fli-1 in wild-type and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 1436)
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THKINPIPPOQEWINOPUNVKREYDHINGSRESPVDCSVGKCNKMVGGTEASOMNY
TGYMDEKCAPPPNMTTNERRVIVPADPSLMSPDHVRQMLDWAIKEYGLQEIDTAMFHS
TDGKELCKMSKDDFLRLTSVYNTEVLLSHLNYLKESSSSLSYNTPSHADQSPRLAAKD
DASYDAVRFGWSNNHHSGKGSPTVYSGSVSKNHPDQFBPKQDLDFYGILGPTSSRLANPG
SGQIQLWQFLLELLSDSANAGCITWEGTNGEFKMTDPDEVARRWGERKSKPNNNYDKL
SRALKXYYDKNIMTKYHGKRYAKFDFHGIAQALQPHPTESTMXXYPSELPYVPSYHA
HQQKVNFVSPHPPSMPVTSSNFFGPTTPYWSSPPGGIYPNPSVPRHANSHVPSHLGSY
Y"
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45. .1400
                                                                                                                                                                                                                                                                                                                                                                                          /product="Fl1-1 protein"
/protein_id="CAB56832.1"
/db_xref="GI:6006477"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="fli-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="20-24hr embryo"
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          MetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisAlaHisProGlnLys
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1359)
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(FLI1) mRNA,
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                                                                                                                                                                                                                                                /translation="MDGTIKEALSVVSDDQSLFDSAYGAAHLPKADMTASGSPDYGQ
PHKIRPLPPQQEWINQPVRVWYKREYDHMNGSRESPVDCSVSKCSKLYGGGESNPMNY
NSYMDEKNGPPPNMTTNERRVIYPADPTLMTQEHVRQWLEWALKEYSLMEIDTSFFQ
NMDGKELCKMMKEDFLARATILXNTEVLLSHLSYLRESGLAYNTTSHTDQSSRLSVK
DPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANK
DPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANK
SGQQIQLWQFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDK
LSRALRYYYDKNIMTKYHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSYH
LSRALRYYYDKNIMTKYHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSYH
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ETS transcription factor; involved in the pathogenesis of Ewings sarcoma following transloc with EWS gene on chromosome 22; may have oncogeniotential when fused with EWS gene"
                                                                                                                                                                                                                             AHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGS
YY "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAK50443.1"
/db_xref="GI:14017403"
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                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAL Plate: 27 Row: g Column: 16
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 2
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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NIH-MGC Project URL: http://mgc.nci.nih.
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/tissue_type="Lymph, Burkitt lym
/clone_lib="NHH_MGC_8"
/lab_host="DH10B-R"_
/product="Unknown (protein for MGC:19589)"
/protein_id="AAH10115.1"
/db_xref="G1:14603316"
/translation="MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQ
                                                                                               /note="Vector: 126. .1484
                                                                            /codon_start=1
                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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NNDGKELCKNMKEDPTLATTLY NTEVLLSHLSY LRESSLLAY NTTSHTDQSSRLSVK
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GSGQIOLGWQFLLELGBDSANASCITWEGTNGEFKMTDPDEVARMGERKSKPMNYDK
LSRALRYYTDKNIMTKVHGKRYAYKFDEFIGIAQALQPPTESSMYKYPSDISMPSYH
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		AHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGS
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Qy	21	CysAlaTyrGlySerProHisLeuAlaLysThrGluMetThrAlaSerSerSerSer 39
Db	186	TCAGCGTACGGAGCGGCAGCCCATCTCCCCAAGGCCGACATGACTGCCTCGGGGGAGTCCT 245
ş	40	GluTyrGlyGlnThrSerLysMetSerProArgValProGlnGlnAspTrpLeuSerGln 59
?	,	
g :	306	CCAGTGAGGGTCAACGTCAAGCGGGAGTATGACCACATGAATGGATCCAGG
Qy	80	AsnSerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsn 99
Дδ	357	GAGTCTCCGGTGGACTGCAGCGTAGCAAATGCAGCAAGCTGGTGGGCGGAGGCGAGTCC 416
Qy	100	ValGlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProProAsnMet 118
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Ωу	w	ValArgGlnTrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeu 158
Ф	537	GTGAGGCAATGGCTGGAGTGGGCCATAAAGGAGTACAGCTTGATGGAGATCGACACATCC 596
Qy	159	LeuPheGlnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArg 178
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Ωу	199	erValTyrProGluAlaThrGlnArgIleTh
뫄	714	AGTTCACTGCTGGCCTATAATACAACCTCCCACACCGACCAATCCTCACGATTGAGT 770
Qy	219	ThrArgProAspLeuProTyrGluGlnAlaArgArgSerAlaTrpThrSerHisSerHis 238
В	771	GTCAAAGAAGACCCTTCTTATGACTCAGTCAGAAGAGGAGCTTGGGGCAATAACATGAAT 830
Qy	239	LysAlaThrGlnProSerSerSerThrValProLysThrGlua
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Best Local Similarity
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P11308;
                                                             Dunn
"ERG
                                                                                                                                                MEDLINE=87317608; PubMed=3476934; Reddy E.S.P., Rao V.N., Papas T.S.;
                                                                                                  CHROMOSOMAL
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                 polyadenylation, and translation."; Science 237:635-639(1987).
                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM ERG-2).
MEDLINE=87263429; PubMed-3299708;
Rao V.N., Papas T.S., Shyam E., Reddy P.;
"erg, a human ets-related gene on chromosome
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcriptional regulator ERG (Transforming pr
                           CHROMOSOMAL TRANSLOCATION
                                                                                   MEDLINE=94356859; PubMed=8076344;
            MEDLINE-94243799;
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                                             T., Praissman L., Hagag N., Viola I gene is translocated in an Ewing's er Genet. Cytogenet. 76:19-22(1994)
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                                                                                                                        erg gene: a human gene related to the ets oncogene."; Natl. Acad. Sci. U.S.A. 84:6131-6135(1987).
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Best Local S
Matches 407
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InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF002198; SAM_PNT; 1.
PfANTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00361; ETS_DOMAIN_3; 1.
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TRANSFAC; T00266; -.
TRANSFAC; T02129; -.
TRANSFAC; T02130; -.
Genew; HGNC:3446; ERG
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DNA_BIND
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An RNA-binding protein gene, TLS/FUS, is fused to ERG in myeloid leukemia with t(16;21) chromosomal translocation. Cancer Res. 54:2865-2868(1994).
-!- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR (BY SIM--!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ERG-1 AND ERG-2 (SHOLD ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML) IS CHURE A CHROMOSOMAL TRANSLOCATION T(16;21)(P11;Q22) WHICL
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EMBL; M21535;
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SIMILARITY: CONTAINS
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               TSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLEL
                                                                        SYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRP------
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TGHGHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLEL
                                                         SYNADILLSHLHYLRETPLPHL---TS--DDVDKALQNSPRLMHARNTDLPYEPPRRSAW
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Watson D.K., Smytn F.L., -----.
Papas T.S., Seth A.;
Papas T.S., Seth A.;
Papas T.S., Seth A.;
The ERGB/Fli-1 gene: isolation and characterization of the family of human ETS transcription factors.";
Cell Growth Differ. 3:705-713(1992).
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  Submitted [8]
                                                                                                                                                 SEQUENCE
Ubhi B.T.
                                                                                                                                                                                        Hromas N., A., Beck E., Klemsz M.J.;
Beck E., Klemsz M.J.;
"Human FLI-1 localizes to chromosome 11q24
transcript in neuroepithalioma.";
transcript in neuroepithalioma. 1;
ciochim. Biophys. Acta 1172:155-158(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93007976; PubMed-1394211; Prasad D.D., Rao V.N., Reddy E.S.; "Structure and expression of human Cancer Res. 52:5833-5837(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                             Strausberg
                                                                                       SEQUENCE
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MEDLINE-92396239; PubMed-1522903;
                                                                 TISSUE-Lymph;
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S., Rainey D.R., Meredith
(APR-2001) to the EMBL/Ge
                       (JUL-2001)
                                                                                                                                                                                                                                                                                               May W.,
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EMBL; X67001; CAA47399.1; -.
EMBL; M9883; AAA35812.2; -.
EMBL; M9883; AAA35817.1; -.
EMBL; M98255; AAA524679.1; -.
EMBL; M93255; AAA58479.1; -.
EMBL; M93255, AAA59443.1; -.
EMBL; M93255, AAA50443.1; -.
EMBL; BC001670; AAH01670.1; -.
EMBL; BC010115; AAH01670.1; -.
EMBL; BC010115; AAH01670.1; -.
EMBL; BC010115; AAH0167.1; -.
EMBL; BC010115; AAH0167.1; -.
EMBL; D38408; BBA07463.1; ALT_TE
PDB; 1FLL; 15-SEP-95.
                                                                                                                                    InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF ETS.
InterPro; IPR0023118; SAM_PNT.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; SAM_PNT; 1.
Pfam; PF00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 276-373:

MEDLIANG H., MAO X., Olejniczak E.T., Nettesheim D.

Meadows R.P., Thompson C.B., Fesik S.W.;

"Solution structure of the ets domain of Fli-1 w

Mat. Struct. Biol. 1:871-875(1994).

-I- FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL

THE DNA SEQUENCE 5'C[CA]GGAAGT-3'.
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Genes Chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 58-452 FROM N.A. MEDLINE-98426231; PubMed-9751743; Zucman-Rossi J., Legoix P., Victo
                                                                                                                                                                                                                                                            Genew; HGNC:3749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                            DOMAIN
                                                         3D-structure.
                                                                     Alternative
                                                                                     Transcription
                                                                                                 PROSITE;
                                DNA_BIND
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Molecular analysis of a t(11;22)
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- SIMILARITY:
- SIMILARITY:
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by non-profit institutions as long as its content is in no
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND BE PRODUCED BY ALTERNATIVE SPLICING.
DISEASE: A FORM OF EWING'S SARCOWA IS CHARACTERIZED CHROMOSOMAL TRANSLOCATION T(11;22)(Q24;Q12) WHICH IN
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                                                                                  PS00345; ETS_DOMAIN_1; 1.
PS00346; ETS_DOMAIN_2; 1.
PS50061; ETS_DOMAIN_3; 1.
ption regulation; Activato
                                                                     splicing; Proto-oncogene;
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361
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                                                                       Activator; DNA-binding;
to-oncogene; Chromosomal
                                                                                                                                                                                                                                                                                                     ALT_TERM.
POINTED.
ETS-DOMAIN.
MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPD
YGQPHKINPLPPQQEWINQPVRVNVKREYDHMNGS -> ME
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translocation
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translocation;
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Best Local
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                                                                        "Erythroleukemia induction by Friend mu
insertional activation of a new member
closely linked to c-ets-1.";
Genes Dev. 5:908-918(1991).
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Li [2] CHARACTERIZATION.
CHARACTERIZATION.
MEDLINE-93275657; PubMed-8502483;
MEDLINE-93275657; PubMed-8502483;
                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Mus musculus (Mouse).
'-rvota; Metazoa; Chordata; '-
                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Friend leukemia integration 1 transcription f
integration site protein Fli-1).
                                                                                                                                                                     STRAIN-BALB/c; TISSUE-Spleen; MEDLINE-91257578; PubMed=2044959; Ben-David Y., Giddens E.B., Letwin
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                 integration site protein FLI1 OR FLI-1.
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 67.0
06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
77
130
133
323
426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
77
130
133
323
426
50982
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67.0%;
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E -> V (IN REF. 5).

MISSING (IN REF. 5).

P -> A (IN REF. 5).

W -> V (IN REF. 5).

E -> Q (IN REF. 4 AND 5).

MISSING (IN REF. 5).

MISSING (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
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                                                                                                                                   new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.367; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1624.5;
Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
        P.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ
                                                                                                                                 murine leukemia virus:
er of the ets gene fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452
                                                                                                                                                                          Bernstein
          Ben-David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
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                                                                                                                                                                                                                                                                                                                                                                                                         factor
                                                                                                                               ets gene
                                                                                                                                                                          Α.,
          Υ.,
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                                                                                                                                                                                                                                                                                                                                                                                                         (Retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                   Euteleostomi;
; Murinae; Mus
          Greer
                                                                                                                                   family, Fli-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452;
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          ъ
                                                                                                                                                                                                                                                                                                     Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALA MARKARA SARAKA SAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000418; Ets.
InterPro: IPR00341; HSF_ETS
InterPro: IPR0033118; SAM_PNT
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig. 1 proto-oncogene, involved in erythroleukemia and Ewing's sarcoma, encodes a transcriptional activator with DNA-binding specificities distinct from other Ets family members."; Oncogene 8:1621-1630(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; Q01543; 1FLI.
TRANSFAC; T01408; -.
MGD; MGI:95554; F111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59421; CAA420
PIR; S17403; S17403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: CAN FORM HOMODIMERS
                                                                                              178
                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                            μ.
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INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLONES F-MULV INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.
DISEASE: INVOLVED IN ERVIHROLEUKEMIA INDUCTION BY FRIENI LEUKEMIA VIRUS (F-MULV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ETS FAMILY.
SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES THE DNA SEQUENCE 5^{\prime}C[CA]GGAAGT-3^{\prime}.
                                                                                                                                                                                                                                                                                                                                                                            SGLNKSPLLGGSQTMGKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSA
                        ATSAYNTEVLLSHLSYLRE--SSLLAYNTTSHTDQSSRLNVKEDPSYDSYRRGAWNNNMN
                                                                                                                   TINERRVIVPADPTLMSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
                                                                                                                                                                                                                                                                                                           PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
                                                                                                                                                                                       TTNERRVIVPADPTLWTQEHVRQWLEWAIKEYGLMEIDTSFFQNMDGKELCKMNKEDFLR
                                                                                                                                                                                                                                                                                   -PVRVNVKREY--DHMNGSRESPVDCSVSKCNKLVGGGEANPMNYNSYMDEKNGPPPPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
281
452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA42055.1;
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361
51002
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1613.5;
Pred. No. 7.9e
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POINTED.
ETS-DOMAIN.
; 1F9A06C6893FE2AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMATOPOIETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETV6/TEL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                     178
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  295
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                                       Query
Best I
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLI1_XENLA STANDARL
P41157;
01-FEB-1995 (Rel. 31, C
01-FEB-1995 (Rel. 31, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                  InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT:
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-94206844; PubMe
Meyer D., Wolff C.M., S
Befort J.J., Remy P.;
"X1-f11, the Xenopus ho
                                                                                                                                                                                                                                                                                                                           entities
or send a
                                                                                                    PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
Transcription regulation; Activator; DNA-binding;
DOMAIN 113 197 POINTED.
                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "X1-fli, the Xenopus homologue of the embryogenesis in a restricted pattern distribution.";
                                                                                                                                                                                                                                                                         EMBL; X66979; CAA47389.1;
HSSP; Q01543; 1FLI.
TRANSFAC; T02067; -.
                                                                              SEQUENCE
                                                                                                                                                                                                                                                             InterPro; IPR000418;
                                                                                                                                                                                                                                                                                                                                                      modified
                                                                                                                                                                                                                                                                                                                                                                    use
                                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviral integration site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XENLA
                Local 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ហ
                                                    Match
                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYO SIMILARITY: BELONGS TO THE ETS FAMILY.

SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGAASQYWTSPTAGIYPNPSVPRHPNTHVPSHLGSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAAPNPYWNSPTGGIYPN---TRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAYKFDFHGIAQALQPHPTETSMYKYPSDISYMPSYHAHQQKVNFVPSHPSSMPVTSSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. 44:109-121(1993).
                                     Similarity
                                                                           282
453 AA;
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8155576;
.M., Stiegler P.,
                                                                           362 E
51015 MW;
                                                                                                                                                                                                                              HSF_ETS.
                                     64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
n site protein Fli-1 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                   .•
                           52;
                        Score 1576; I
Pred. No. 4.26
2; Mismatches
                                                                         ETS-DOMAIN.
; A6E6FCC60EC42DA4 CRC64;
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evocative of neural crest
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PROSITE;

PS00345; PS00346;

ETS\_DOMAIN\_1;
ETS\_DOMAIN\_2;

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RESULT 6
ERG_MOUSE
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P81270;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                       InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00178; Ets; 1.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                              gene
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                                                                                              EMBL; S66169; AAB28525.1; HSSP; Q01543; 1FLI.
                                                                                                                                       entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-94019387;
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional regulator ERG OR ERG-3.
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                                                                                MGD; MGI:95415; Erg.
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                                                                                                                                                                                                                                                   e expression.";
Cell. Biol. 13:7163-7169(1993).
FUNCTION: ACTS AS A TRANSCRIPTIONAL
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE ETS FAMIL
                                                                                                                                                                                                                                                                                                                         INE-94019387; PubMed-8413305; ra R.R., Stuiver M.H., Steenb proteins: new factors that r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKSIMTKVHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPYTKSPPMGGTQNVNKSGDQQRSQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDS
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                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                    FAMILY.
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Transcription
NON_TER
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Q01414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                     "The sea urchin
                                     InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS
Pfam; PF00178; Ets; 1.
                                                                             EMBL; M81067; AAA68905.1;
HSSP; Q01543; 1FLI.
                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           DNA Seq. 3:127-129(1992).
-i- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACT-
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                         MEDLINE=93091246; PubMed=1457815;
Q1 S., Chen Z.Q., Papas T.S., Lautenberger J.A.;
"The sea urchin erg homolog defines a highly con
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Transcriptional regulator ERG homolog (Fragment).
                           SMART; SM00413; ETS;
                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata;
                                                                                                                                                                                                                                                                                                                                                                           Lytechinus
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 PS00345;
PS00346;
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272 AA;
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regulation; Activator; Nuclear
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ETS_DOMAIN_1;
ETS_DOMAIN_2;
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85.3%;
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a; Temnopleuroida; Toxopneustidae;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Goodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.Y., Mobarry C., Scheeler F., Shen H.,
RA Rainer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Rainer E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Rainer E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Sing R., Sta
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Ol-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
DNA-binding protein D-ETS-6.
ETS-21C OR ETS-6 OR CG2914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50061; ETS_DOMAIN_3; 1.
Transcription regulation; Activator; Nuclear NON_TER 1 1 1 1 ETS-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETS6_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
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173 AA;
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19690 MW;
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73.3%;
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Pred. No. 2.
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; F85D496DD58A8F3D CRC64;
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.2e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_NT; 1.
SPROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
"Iso]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00178; Ets; 1. Pfam; PF02198; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev.
                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000418; InterPro; IPR002341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0005660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q01543; 1FLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M88475; AAA284!
PIR; S28823; S28823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003118;
                                             183
                                                                                                    123
                                                                       163
                                                                                                                                                                                                                                                  43
                                                                                                                                                             69
                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hen T., Bunting M., Karim F.D., Thummel C.S.;
solation and characterization of five Drosophila genes
ets-related DNA binding domain.";
blol. 151:176-191(1992).

SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EMBRYCOMIC VENTRAL NERVOUS SYSTEM A
NEURONS IN EACH THORACIC SEGMENT.
DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT
SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: Ref.2 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frameshift in position 242.
LPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGS-G
                                                                                                                                                                                                                QSHKQLPIISQTIRSAWCQQRPINAMHQDVRQKSIGSGNETKLEAKETEVPTNRRRRRRR
                                                                                                                                                                                                                                               QTSKMSPRVPQ---QDWLSQPPARV------TIKMECNPNQV-NGSRNSPDD
                                                                                                    SPHQAPSPRRNSSDSNRSVSPVEVPVDPHAWTPEDIASWVRWATRKFKLDPEPDIDRFPK
                                                                                                                                                                                         CSVAKGGKMVSSSDNVGMNY-----GSYMEEKHI------
                                                                 IDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPD
                                                                                                                               -PNMTTNERR-----VIVPADPTLWSTDHVRQWLEWAVKEYGL-PDVDILLFQN 162
                                          -DAQELCDLSRADFWVCAGSRRGGMLLAQ-HFA-----ISLY-HATGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE003589; AAF51484.1; -.
                                                                                                                                                                                                                                                                                             Similarity
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475 t
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA28452.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                      A.
                                                                                                                                                            -STSDSSASSYSSTDSDSGSSTSSSSIRSQLPALNLPVPLPLATPTPPAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=1577186;
                                                                                                                                                                                                                                                                                                                                                     ir protein
335
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                                                                                                                                                                                                                                                                                            24.5%;
                                                                                                                                                                                                                                                                                                                                        51802 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ets21C.
                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                            Score 599; DB 1;
Pred. No. 3.2e-36;
                                                                                                                                                                                                                                                                                                                                 ETS-DOMAIN.
; 0D382C41C03B1502 CRC64;
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                                                                                                                                                                                                                                                                              124;
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                                                                                                                                                                                                                                                                                                         Length 475;
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RESOLUTION OF THE PROPERTY OF 
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RX MEDLING-20196006; PubMed-10731132;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li.P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ghorit S., Banker E.G., Ferriara S., Fleischmann W.,
RA Borkova D., Evaley S., Dahlke C., Davenport L.B., Davies P.,
RA Ghorit S., Bayraktaro C.D., Ferriara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Molaris J., Katchum K.A.,
RA Mount S.M., Molaris H., Gu S., Pacleb J.M.,
RA Mount S.M., Molaris H., Gu S., Pacleb J.M.,
RA Ra Ballew R.
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                                                                   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhang Zhang X.H., Zhong F.N., Zhong W., Zhan M.S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-CCT-2001 (Rel. 40, Last sequence
15-JUN-2002 (Rel. 41, Last annotatio
DNA-binding protein D-ETS-3.
ETS65A OR ETS3 OR CG7018
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P29774; Q9VRU5;
01-APR-1993 (Rel.
           SEQUENCE
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       FROM
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TISSUE SPECIFICITY, AND
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Best Local S
Matches 114
                                      Q00422;
Q00422;
Q1-DEC-1992 (Rel. 24, Last sequence update)
Q1-DEC-1992 (Rel. 24, Last sequence update)
Q1-DEC-1992 (Rel. 41, Last annotation update)
Q2 binding protein alpha chain (GABP-alpha subunit).
Q2 binding protein alpha chain (GABP-alpha subunit).
Q3 binding protein alpha chain (GABP-alpha subunit).
Q4 binding protein alpha chain (GABP-alpha subunit).
Q5 binding protein alpha chain (GABP-alpha subunit).
Q6 binding protein alpha chain (GABP-alpha subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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STRAIN=Canton-S; TISSUE=Larva;
MEDLINE=92249640; PubMed=1577186;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00178; Ets; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003563; AAF50695.1; -.
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TISSUE SPECIFICITY: EMBRYONIC VENTRAL
THE THORACIC THAN ABDOMINAL SEGMENTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - FMTPYHHSAKLSSFMSPH - HGMTSSSASIFPSAASWGNWGSPATNLYQPHSMSHVTPSH
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Q01543; 1FLI.
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IPR002341; HSF_ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AA;
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                                                                                                                                                                                                                                                                                                                      STANDARD;
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25; Mismatches
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; 3F8AD7D0C88BCE8B CRC64;
                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                         454
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Best Local S
Matches 123
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Science
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SMART; SM00413; ETS; 1.
SMART; SM002413; ETS, NI; 1.
SMART; SM00251; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use as long as its content use as long as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; DNA-binding; DOMAIN 170 251 POINTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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RICH REPEATS (GA REPEATS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) MEDLINE-98128030; PubMed-9461436;
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Pfam; PF02198; SAM_PNT; 1.
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-!- SIMILARITY: BELONGS TO THE ETS
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Wolberger C.;
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"Identification of Ets-and notch-related subunits in GA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=91343912; PubMed=1876836;
      237
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SHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPG---
                                                                   RVP--RGEILWSHLELLRK--
                                                                                                                               LTPSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARR--SAWTSH
                                                                                                                                                                                            RKEQERLGIPYDPIRWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQ
                                                                                                                                                                                                                                                                                                                            ---AHHAEAEAHLVEEAQVITLDGT------KHITTISDETSEQVTRWAAALEGY 173
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454 AA;
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30.1%;
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                                                                                                                                                                                      EMBL; D13318; BAA02575.1; -
EMBL; U13044; AAA65706.1; -
HSSP; Q00422; 1AWC.
TRANSFAC; T01390; -
Genew; HGNC:4071; GABPA.
MIM; 600609; -
                  PRINTS;
SMART; S
SMART; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GABA_HUMAN STANDARD; PRT; 454 AA. Q06546; Q1939; Q16546; Q1939; Q1-FEB-1995 (Rel. 31, Created) Q1-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) GA binding protein alpha chain (GABP-alpha subunit) (Transcription factor E4TF1-60) (Nuclear respiratory factor-2 subunit alpha).
                                                                                                                                                                                                                                                                                                                                                                                                            use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95097980; pubMed=7799916; Gugneja S., Virbasius J.V., Scarpulla R.C.; "Four structurally distinct, non-DNA-binding subunits nuclear respiratory factor 2 share a conserved transcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                     InterPro; IPR000418; InterPro; IPR002341; InterPro; IPR0023118;
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                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLI. Biol. 15:102-111(1995).

FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF IN RICH REPEATS (GA REPEATS). NECESSARY FOR THE ADENOVIRUS E4 GENE.
SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO SUBCELLULAR LOCATION: Nuclear.

SIMILARITY: BELONGS TO THE ETS FAMILY.
SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                 PF00178;
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PF002198; SAM_PNT; 1.
S; PR00454; ETSDOMAIN.
SM00413; ETS; 1.
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                                                                                                                                                                                                                                                                                                               non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
  PS00345;
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ETS_DOMAIN_1;
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O1-JUN-1994 (Rel. 29, Create
O1-JUN-1994 (Rel. 29, Last s
15-JUN-2002 (Rel. 41, Last a
DNA-binding protein D-ELG.
ETS97D OR ELG OR CG6338.
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
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Q04688; Q9
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=93096481; PubMed=1461651;

The S.M., Xie X., Smyth F., Papas T.S., Watson D.K., Sc)

"Molecular characterization and structural organization
ets proto-oncogene-related gene of Drosophila.";

Oncogene 7:2471-2478(1992).
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ETS_DOMAIN_3;
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ETS-DOMAIN.
SS -> RC (II
A -> V (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 460; DB 1;
Pred. No. 3.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Þ
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1AF2ABBBC79191DD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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ion of D-elg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexapoda;
                                                         s G.L.c
                                                                                                                                                                                                                                                                                                                                                                                                             R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RA Harris N.L. Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Liu X., Mattei B., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Mchulov G., Milshina N.V., Nobarry C., Morris J., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shaith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
                                                                                                                                                                                                                             EMBL;
PIR;
                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Canton-S; TISSUE=Larva; MEDLINE=92249640; PubMed=1577186; Chen T., Bunting M., Karim F.D., Thummel C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pribyl L.J., Watson D.K., Schulz R.A., "D-elg, a member of the Drosophila ets expression and evolutionary comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burtis
Cherry
                                                           TRANSFAC; T02085;
FlyBase; FBgn0004
                                                                                                                                                                                                                                                                                                                                                           EMBL; X68259;
                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 6:1175-1183(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 323-463 FROM N.A. MEDLINE-91319397; PubMed-1713660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., D. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 298-449 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ets-related DNA binding domain.";
v. Biol. 151:176-191(1992).
                                                                                                                                                    IL; AE003758; AAF56638.1;

IL; XS8481; CAA41390.1; AL5

IL; MB8471; AAC34199.1; -

IL; S24300; S24300.

IL; S28822; S28822.

IL; S37616; S37616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEVELS DURING LARVAL DEVELOPMENT.
SIMILARITY: BELONGS TO THE ETS FAMILY.
SIMILARITY: CONTAINS 1 POINTED (PNT) D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: UNIFORM DISTRIBUTION THROUGHOUT EMBRYONIC DEVELOPMENT, WITH SLIGHTLY HIGHER EXPRESSION IN POLE CELLS. DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER LEVELS DURING LARVAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MAY HAVE A ROLE IN GERMLINE DEVELOPMENT. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.C., Busam I
J.M., Cawley
   FBgn0004510; Ets97D.
; IPR000418; Ets.
; IPR002341; HSF_ETS.
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                                                                                                                                                                                                                                                                                                                                                           CAA48327.1;
Ets.
HSF_ETS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib
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gene f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s T.S.; family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dew I., Dietz
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uri V., Reese M.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q., Zheng L., X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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                                                                                                                                                                                                                                                                                                                                         RESULT 13
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Best Local
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Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                01-NOV-1990
01-NOV-1990
15-JUN-2002
                                                                                            MEDLINE=90384849; PubMed=2205841;
Stiegler P., Wolff C.M., Baltzinger M.,
Meyer D., Chysdael J., Stehelin D., Befo
"Characterization of Xenopus laevis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_3;
PROSITE; PS50061; ETS_DOMAIN_3;
DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                   C-ETS-1A protein.
                                                                                                                                                                                                                                                                                                      P18755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                      Nucleic
                                                                                oncogene."
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                              Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                      Amphibia; Batrachia;
                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                           ETS-1A.
                                                                                                                                                                                                                                                                                                                ETIA_XENLA
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                                                                                                                                                                                                                                                                                                                                                                            420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 NQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPP-----PNWTTNERRV 125
      SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; C-ETS-1A (SI ETS-1A', ARE PRODUCED BY ALTERNATIVE SPLICING SIMILARITY: BELONGS TO THE ETS FAMILY.
SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                             RFAYKFD
                                                                                                                                                                                                                                                                                                                                                                                                    RYAYKFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TQSKATQPSSSTVPKTEDQRPQLDPYQILGPTS-SRLANPGSGQIQLWQFLLELLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIFWTHLQLLKE--CNFV---SVVHKRAEEQ--RKPKQPRIMSANSISTNSGGSLSLEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILLSHLHYLRERGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIPEAANEWTHAHVIYWLEWAVKQFELVGINMSDWQ-MNGQELCAMTHEEFNQKLPRDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQKSSSSESPIKTPLKRMHKEDSEEESV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMRKSYQSVKSSDSVESTTSS------MNPSNYTTIGSGNNGQVQLWQFLLEILTDC
                                                                     Acids Res. 18:5298-5298(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                              (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA;
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454
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                                                                                                                                                                                          Xenopus
                                                                                                                                                                                                                                                                                                                 STANDARD;
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454
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                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52658 MW;
                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETS-DOMAIN.
L -> V (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454.5;
No. 9.
                                                                                             M., Hirzlin J.,
Befort N., Remy
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Best Local S
Matches 119
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Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETS_DMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1
PROSITE; PS00346; ETS_DOMAIN_2; 1
PROSITE; PS00346; ETS_DOMAIN_3; 1
PROSITE; PS00346; ETS_DOMAIN_3; 1
                                         ETS1_HUMAN
P14921;
01-APR-1990
01-APR-1990
16-OCT-2001
  C-ets-1
ETS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52692;
PIR; S11225; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC; T02040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000418;
InterPro; IPR002341;
InterPro; IPR003118;
                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                              305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
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                                                                                                                                                                                                                                                                     DFHGIAQALQPHPPE
                                                                                                                                                                                                                                                                                                                                   TGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKTAGKRYYYRFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKEQQRLGIPIDPREWIDMHVREWVSWAVNEFILKGVDFQKF-CMSGAALCALGKECFLE
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                                                                                                                                                                                                                                              DL---
                                                                                                                                                                                                                                                                                                                                                       EGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKF--
                                                                                                                                                                                                                                                                                                                                                                                                                     SHKSKGTFKDYVRDRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLGRISRGKLGGQESFESIESHDSCDRLTQSWSSQSSYNSLQRVPSYDSFDSEDYPPAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSFITESYQTLHPISSEELLSLKYENDYPLGLLRDPLQPESLQGDYFTIKQEVVTPDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAPDFVGDILWEHLEILQKDSKQYQTSEITPAYPESRYTSDYFISYGIEHAQCVPPSEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTPSYNADILLSHLHYLRERGATFIFPN-TSVYPEA------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P14921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il Similarity
119; Conserv
                    protein
                                                                                                                                                                                                                                              -QSLLGYVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438
                                           (Rel. 14,
(Rel. 14,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Nuclear
51 13
332 41
153 15
279 27
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$11225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ,
                                                                                                                                    STANDARD;
                      (p54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARRSAWTSHSHPTQSKATQPSSS-----TVPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSF_ETS.
                                                                                                                                                                                                                                                                                         377
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                                                                                                                                                                                                                                              424
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                                           Last sequence up
                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DLPYEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 451.5;
Pred. No. 1.4e
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POINTED.

ETS-DOMAIN.

PHOSPHORYLATION (BY CAMK) (POTENTIAL).

PHOSPHORYLATION (BY CAMK) (POTENTIAL).

MISSING (IN ISOFORM C-ETS-la').

B97a8EBDF2DB51FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITW
                                                                                                                                  441
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1.4e-25;
hes 96;
                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
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EMBL; X14798; CAA32904.1; EMBL; X14798; CAA32903.1; EMBL; X14798; CAA32903.1; EMBL; 304101; AAA52410.1; PIR; A32066; TVHUET PIR; S10086; S10086
                                                                                                                                                                                                                                                                                              InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR0033118; SAM_PNT;
InterPro; IPR003118; SAM_PNT;
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 2STT; 12-MAR-97.
PDB; 2STW; 12-MAR-97.
TRANSFAC; T00112; -.
TRANSFAC; T01400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Werner M.H., Clore G.M., Fisher C.L., Shiloach J., Gronenborn A.M.;
"The solution structure of the human mode of binding and true side chain i Cell 83:761-771(1995).
       DNA_BIND
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMK OF JULY 1996 MEDLINE-96097120; PubMed-8521493; MEDLINE-96097120; MEDLINE-9609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watson D.K., McWilliams M.J., Lapis P., Lautenber Schweinfest C.W., Papas T.S.; Manmalian ets-1 and ets-2 genes encode highly coproc. Natl. Acad. Sci. U.S.A. 85:7862-7866(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89042086; Watson n ...
                                                                                                                                                                                   PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -11 SUBCELLULAR LOCATION: Nuclear:
1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; C-ETS-1A (SHOWN
1B; ARE PRODUCED BY ALTERNATIVE SPLICING.
1- PTM: ISOFORMS OF ETS-1 ARE ALSO GENERATED BY DIFFE
                                                                                    Phosphorylation;
DOMAIN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 164720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                            Proto-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure, expression and alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reddy E.S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=89083219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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PHOSPHORYLATION.

DISEASE: ETS IS RESPONSIBLE FOR ERYTHROBLAST TRANSFORMATION. THE JUXTAPOSITION OF THE INTETRANSFORMATION. MAY BE INVOLVED IN THE PATHOGI
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een the Swiss Institute of Bio
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Matches 114;
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                                                                                                                                       SEQUENCE FKUM N.S.

STRAIN-BALB/C; TISSUE-Thymus;

MEDLINE-90299137; PubMed-2163347;

MEDLINE-90299137; PubMed-2163347;

Gunther C.V., Nye J.A., Bryner R.S., Graves B.J.;

Sequence-specific DNA binding of the proto-oncoprotein ets-1 a transcriptional activator sequence within the long terminal a transcriptional activator sequence within the long terminal
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                         Chen
                                                                       SEQUENCE FROM STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                            of 50
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Watson D.K., Seth A.,
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ETS1 OR ETS-1.
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                                                   MEDLINE=90370376;
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                                                                                                                                                                                                                                                                                                                                                                 IN-BALB/c; TISSUE-Fibroblast; on D.K., Seth A., Smyth F.E., Schweinfest C.W., Papas T.S.; chicken, mouse and human ETS-1 proteins all have predicted 0 kDa, but have different electrophoretic mobilities."; Papas T.S. (eds.); Papas T.S. (eds.);
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MISSING (IN ISOFORM C-ETS-1B).
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of mouse c-ets-1
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SMART; SM00251; SAM_PNT; 1.
SMART; SM00251; SAM_PNT; 1; 1
PROSITE; PS00345; ETS_DOMAIN_2; 1
PROSITE; PS00346; ETS_DOMAIN_2; 1
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PIR; A30487; A30487.
PDB; 1ETC; 29-JAN-96.
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MEDLINE-98445336; PubMed-9770451;
Slupsky C.M., Gentile L.N., Donaldson L.W., Mackereth C.D.,
Seidel J.J., Graves B.J., McIntosh L.P.;
"Structure of the ets-1 pointed domain and mitogen-activated protein kinase phosphorylation site.";
Proc. Natl. Acad. Sci. U.S.A. 95:12129-12134(1998).
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EMBO. J. 15:125-134(1996).
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE ETS FAMILY.
-i- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
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s. 5:277-285(1990).
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
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-Q-/cgn2_1/USPTO_spool/US09902772/runat_07112002_134033_9021/app_query.fasta_1.1294
-DB-M_Geneseq_10102 -QFMT-fastap -SUFFIX-rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=200000000
-USER-US09902772_eCGN_1_1_103_evrunat_07112002_134033_9021 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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## RESULT 1 AAXZ6551 ID AAXZ6551; XX AAZ26551; XX AAZ26551; XX AXZ6551; XX DT 14-JUN-1999 (first entry) XX DE DNA encoding chicken C-11 protein. XX Chicken; C-11 protein; cell calcification inhibiting agent; c-erg protein; arthritis XX XX CS call calcification inhibiting agent; c-erg protein; arthritis XX CS Gallus sp. XX CS Gallus sp. XX CDS Gallus sp. Location/Qualifiers FT CDS 63..1418

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                                                                                                                                                                                                                                                                                                                                                                    Sequence
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18-JUN-1997;
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                      encoding chicken c-erg
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                                                                                             TyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisAlaHisProGlnLysMet
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                          An active protein for inhibiting cell calcification - useful fineasuring the calcification of a cell, for diagnosing arthritis deformans or ossification of spinal column ligament
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18-JUN-1997;
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(UYPE-) UNIV PENNSYLVANIA.
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	roAsnThrArgLeuProAlaAlaHisMetProSerHisLeuGlyThrTyrTy		Qy
1442	TCATCCAGCTTTTTTGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTAC	1383	В
433	erSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleT	414	δÃ
1382	CATGCACACCCCCAGAAGATGAACTTTGTAGCTCCCCATCCCCCTGCTTTGCCCGTAACC		皮
413	isAlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuPro	394	Qy
1322	CACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTAC	1263	망
393	isProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTy	374	Qγ
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7	isGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnPr	354	Ş Q
<b>ં</b>		1143	밁
353	yrAspLysLeuSerArgAlaLeuArgTyrTyrTyrAspLysAsnIleMetThrLysVa	334	Qy
1142	ACAGACCCTGATGAAGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAAC	1083	밁
333	${\tt AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAs}$	314	Qy
1082	TCGGACAGCTCCAACTCCATCACCTGGGAGGGCACAAATGGGGAGTTCAAGATG	1023	Db
313	erAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMe	294	Qy
1022	CGTCTTGCAAATCCAGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTG	963	DЬ
293	rgLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLe	274	Qy
σ	AAAACAGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCTTGGACCGACC	903	Db
	${ t sThrGluAspGlnArgProGlnLeuAspProTyrGlnIleLeuGlyProThrSerSet}$	254	Qy
902	ACGAGTCACAGCCATCCCACTCAGTCAAAAGCTACCCAACCATCATCTTCAACAGTGCCC	843	В
253	SerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSerThrValPr	234	Qy
842	ACGCAAAGAATAACAACAAGGCCAGATTTACCTTATGAGCAAGCGAGGAGATCAGCGTGG	783	Дb
233	$hr {\tt GlnArgIleThrThrArgProAspLeuProTyrGluGlnAlaArgArgSerAlaTr}$	214	Qy
782	ij	723	DЪ
213	GlyAlaThrPheIlePheProAsnThrSerValTyrProGluAl	199	Qy
722	ACATTTGACTTCAGATGATGTTGATAAGGCCTTACAAAACTCTCCACGGTTAATGCA	663	Дb
198		198	Qy
662	AGATATCCTCCTGTCACACCTACACTACCTCAGAGAGACTCCTCT	603	Дb
198	roSerTyrAsnAlaAspIleLeuLeuSerHisLeuHisTyrLeuArgGluArg	181	Qy
602	CAGAACATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACG	543	DЬ
180	lnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuT	161	Qy
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160	lnTrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeu	141	Qy
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                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                           New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma
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         The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression and comparing CC the expression level in an unactivated CC (GC, where differential expression of GS is indicative of GCA. CC Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in GS; (2) screening (M3) CC chronic) in a tissue, an altergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an altergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an altergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an altergic response in a subject, exposure of a consideration (M5) an inflammation (especially chronic) or in a tissue, an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue having constanting GA; M3 is useful for detecting a tissue having condulating GA; M3 is useful for screening an agent capable of modulating CC detecting an inflammation in a tissue; M4 is useful for detecting an inflammation in a figure in a pathogen in a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic detecting an inflammation in a tissue; M4 is useful for detecting GC detecting an allergic response in a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic detecting GC detecting GC detection and inflammation in a tissue, an allergic detecting GC detection and in a detection in a detection in a dete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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 Nojima H, Yoshisue
Kuga T, Sekine S,
                                                                                                         arteriosclerosis;
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                     (KYOW )
                                        01-OCT-1999;
                                                     02-OCT-2000;
                                                                               WO200125427-A1
                                                                                            Homo sapiens.
                                                                                                               Human; shear stress-response
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NOJIMA H.
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  H, Obayashi
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 462-466;
                                                                                                                                                                                                                                                                                                                                                                      Sequence
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P-PSDB; AAB90792.
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encoded by them and antibodies against treatment of vascular disease caused by γď

The present invention provides the protein and coding sequences number of human shear stress response proteins. These are useful diagnosis, treatment and screening of vascular diseases caused t arteriosclerosis, including heart failure, post-PTCA restenosis aused by of. in the a

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Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2954 304 57 84 12

TCAGCGTACGGAGCGCAGCCCATCTCCCCAAGGCCGACATGACTGCCTCGGGGAGTCCT 

GluTyrGlyGlnThrSerLysMetSerProArgValProGlnGlnAspTrpLeuSerGln 352 59

ProProAlaArgValThrIleLysMetGluCysAsnProAsnGlnValAsnGlySerArg 79 403

GAGTCTCCGGTGGACTGCAGCGTTAGCAAATGCAGCAAGCTGGTGGGCGGAGGCGAGTCC AsnSerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsn 99 463

ValGlyMetAsnTyrGlySerTyrMetGluGluLysHis---IleProProProAsnMet 118 523

LeuPheGlnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArg 178
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TTTTTCCAGAACATGGCTAAGGAACTGTGTAAAATGAACAAGGAGGACTTCCTCCGC 703

GlyAlaThrPheIlePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThr

AGTTCACTGCTGGCCTATAATACAACCTCCCACACCGACCAATCCTCACGATTGAGT 238

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RESULT 6
AAO5062
ID AAO55
XX AAO55
XX AAO55
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XX Chro
DE Huma
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                                                                                                                                  Ews gene; malignant melanoma; hum-fli-1; primitive peripheral neuroectodermal tumour; human chromosome
                                                                                                                                              chromosomal translocation; chimeric; chimaeric; Ewing sarcoma;
Ews gene; malignant melanoma; hum-fli-1;
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|CAACGGCCCCAGCCAGATCCGTATCAGATCCTGGGCCCGACCAGCAGTCGCCTAGCCAAC
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The intron-exon junctions of the human Ews gene and the Hum-F11-1 gene have been sequenced (see AAQ50646 and AAQ50662, respectively). The different fusion products which could be formed by fusing exons from the two genes, as happens after specific chromosomal translocations, can be predicted (see AAQ50671-Q50678). The sequence
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P-PSDB;
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                                               Disclosure;
                                                              New nucleic acid of EWS gene and its sequence involved in chromosomal transvenant, probes, fusion proteins etc., of Ewing sarcoma and melanoma
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                                                                                      183
                                                                                                       685
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                                                                                                                                                                                                                                                                                   AlaThr --
                                                                            TyrAsnAlaAspIleLeuLeuSerHisLeuHisTyrLeuArgGlu------ArgGly
                                                                                                                 ValThrIleLysMetGluCysAsnProAsnGlnValAsnGlySer--------
                                                                                                                                                                                                                                                                                                                                                                                          GCGGCAGCCCATCTCCCCCAAGGCCGACATGACTGCCTCGGGGAGTCCTGACTACGGGCAG
TATAATACAACCTCCCACACCGACCAATCCTCACGATTGAGTGTCAAAGAAGGTAAGTTT
             ProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgPro----
                                 AGTACCCAGGGCTGGGGTTATAACCTGTTTATGTTTTGCCTCTCAGGTTCACTGCTGGCC
                                                                   ATGGATGGCAAGGAACTGTGTAAAATGAACAAGGAGGACTTCCTCCGCGCCACCACCCTC
                                                                                                                                                                                                               AGGAGAGTCATCGTCCCCGCAGGTAATTCGAGAACCAGGCTGCCTGGGCGCCTCCTTGCT
                                                                                                                                                                                                                          GCCTGTGCAGGATTGGGCCTTGGGCTTTTGCCCCCTCCTCACTTTAGGGAGTCTCCGGTG
                                                                                                                                                                                                                                                                                                                                                        GTCAACGTCAAGCGGGAGTAT-----GACCACATGAATGGATCCAGGTAAGCTCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SerProHisLeuAlaLysThrGluMetThrAlaSerSerSerSerGluTyrGlyGln
                                                                                                                                                                                                                                                                                                                                       -----ArgAsnSerProAsp
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1506.50
62.10%
52.45%
61.64%
                                                  -PheIlePhe-----
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310
57
77
147
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	ACCCACGTGCCTTCACACTTAGGCAGCTACTAC 1857	1825	Db
	AlaHisMetProSerHisLeuGlyThrTyrTyr	4.4	Qy
1824	CTGGACCTCCCCCACGGGGGAATCTACCCCAACCCCAACGTCCCCCGCCATCCTAAC	σ	Db
4	ThrArgLeuProAla	42	y Qy
1764	GCATCACAA	1705	рь
423	roHisProProAlaLeuProValThrSerSerPhePheAlaAlaProAsnPro	404	Qy
1704	TCCTACATGCCTTCCTACCATGCCCACCAGCAGAAGGTGAACTTTGTC	1645	Db
403	ProTyrMetSerSerTyrHisAlaHisProGlnLysMetAsnPheVal	384	Qy
1644	CACGGCATTGCCCAGGCTCTGCAGCCACATCCGACCGAGTCGTCCATGTACAAGTAC	1585	ઠ
383	heHisGlyILeAlaGlnAlaLeuGlnProHisProProGluSerSerMetTyrLysTyr	364	Qy
1584		1525	ф
363	TyrTyrAspLysAsnIleMetThrLysValHisGlyLysArgTyrAlaTyrLysPheAsp :	344	Qy
1524	GGCGAGCGGAAAAGCAAGCCCAACATGAATTACGACAAGCTGAGCCGGGCCCTCCGTTAT	1465	Дb
343		324	Qy
1464	TGG	1405	망
323	rpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAlaArgArgTrp	304	Ωу
1404	CAGCTGTGGCAATTCCTCCTGGAGCTGCTCTCCGACAGCGCCAACGCCAGCTGTATCACC	1345	Db
303		284	Qy
1344	GCCTGCAAGCCTTTTTTGTTCTCTCCCCGTTTCCTCACGGCGTGCAGGAAGCGGGCAGATC	1285	Db
283	Ile	279	Qy
1284	TTTACCTTG	1225	В
278		264	Qy
1224	ACCTGCCCAGGATATGTAATCTCTCCTTTGAAGCAAATTTCCTTTTTTATTTCCTTAGAT	1165	рь
263	۵-	262	Qy
1164	CCTCCCCTTGGAGGGGCACAAACGATCAGTAAGAATACAGAGCAACGGCCCCAGCCAG	1105	рь
261	roSerSerSerThrValProLysThrGluAspGlnArgProGln	247	Qy
1104	AAGTAAATGTTTTATAGTTCTTTGGAGGCTCACTGCATTTCTTTC	1045	চ
246	Gln	244	Ωу
1044	ATGACTCAGTCAGAAGAGGAGCATGGGGCAATAACATGAATTCTGGCCTCAACAAAAGT	.985	Дb
243	luGlnAlaArgArgSerAlaTrpThrSerHisSerHisProThrGlnSerLys	225	Qy
984	CCCTTCT	925	рь
224	AspLeuPro	222	Qy

RESULT 7
ABA48124/c
ID ABA48124 standard; D
XX
AC ABA48124;
XX
DT 01-FEB-2002 (first
XX

DNA; 567 ВÞ

(first entry)

Human breast

cell single

exon nucleic

acid

probe

#6819

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
Score:
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                                                                                                                                     US-09-902-772-2
                                                                                                                                                                                                                                                                                                             CC from human breast and BY 474 cells. The method involves contacting cc the probes with a collection of detectably labelled nucleic acids cc derived from mRNA of human breast, and then measuring the label cc bound to each probe of the microarray. The probes are useful for cells are useful for yearifying the expression of regions of genomic DNA predicted to ce encode proteins. They are useful for gene discovery, and for ce encode proteins. They are useful for gene discovery, and for ce expression analysis is useful for assessing the toxicity of chemical catermining predisposition and/or prognosing breast disease. Gene ce expression analysis is useful for assessing the toxicity of chemical catermining probes for measuring gene expression, with far less bias ct than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the invention is the properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                           Sequence 567
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                            474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spatially-addressable set of single exon nucleic acid puriful for measuring gene expression in sample derived from ast, comprises number of single exon nucleic acid probes
                        WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                     (1-451) x ABA48124 (1-567)
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236236359.
                                                                                                                                                                                                                                                                         BP; 114 A; 124
                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n relates to a spatially-addressable set of single exon probes for measuring gene expression in a sample derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 6819; 327pp + sequence listing; English
                                                                                                                                                               2.91e-71
948.00
97.74%
95.48%
38.79%
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                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                               567
169
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334
                          415
                                                    314
                                                                               475
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RESULT 8
ABA66003/c
ID ABA660
XX ABA660
XX ABA660
XX Human
DT Ol-FEB
XX Human;
XX Human;
XX Homo s
XX Human
PR 21-SEP
PR 21-SE
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  measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probe for measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnThrArgLeuProAlaAlaHisMetProSerHisLeuGlyThrTyrTyr
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                                                                                                                                                                                                             genome-derived single exon nucleic zing gene expression in human fetal
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2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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The sequence

format directly

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ABA33090/
ID 3BA3
XX ABA3
AC ABA3
AC ABA3
AC ABA3
XX ABA3
AC ABA3
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AC ABA3
AC A
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                                                                                                                                                                                                                                                 Human; gene expression; h cardiovascular disease; h congenital heart disease;
                            30-JAN-2001; 2001WO-US00666
                                                                                09-AUG-2001.
                                                                                                                                                                                             Homo sapiens.
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                            gene expression analysis
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95.48%
38.79%
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                                                                                                                                                                                                                                                                           hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                        heart; microarray; vascular system; probe;
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Alignment
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26-MAY-2000; 2000US-0508408.
30-JUN-2000; 2000US-0532366.
21-SEP-2000; 2000US-0536359.
21-SEP-2000; 2000US-0236487.
27-SEP-2000; 2000US-0236359.
04-0CT-2000; 2000GB-0024263.
                                                                                                                                               measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, mentioring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Single
hearts
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                                            Sequence 567 BP;
                                                                                                            Note: The sequence data for this patent did not specification, but was obtained in electronic fo
                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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Scores:
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                                          114 A;
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Percent Similarity:
Best Local Similarity:
Query Match: 2.91e-71 948.00 97.74% 95.48% 38.79% Conservative: Mismatches: Indels: Length: Matches:

Gaps:

400

169

(1-451)x ABA33090 (1-567)

Qγ	275	LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSer 294	
B	534	CTGACCTCATTAGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCCTGGAGCTCCTGTCG 475	
Qy	295	AspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThr 314	
Вb	474	GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG 415	
Qy	315	AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr 334	
뮹	414	GATCCCGACGAGGTGGCCCGGCGCTGGGGAAGAGCGGAAGAGCAAACCCAACATGAACTAC 355	
Qy	335	AspLysLeuSerArgAlaLeuArgTyrTyrAspLysAsnIleMetThrLysValH1s 354	
DЬ	354	GATAAGCTCAGCCGCGCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCAT 295	
Qy	355	GlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnProHis 374	
DЬ	294	GGGAAGCGCTACAAGTTCGACTTCCACGGGATCGCCCAGGCCCTCCAGCCCCAC 235	
Qy	375	ProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrH1s 394	
дb	234	CCCCCGGAGTCATCTCTGTACAAGTACCCCTCAGACCTCCCGTACATGGGCTCCTATCAC 175	
Qy	395	AlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThrSer 414	
Db	174	GCCCACCCACAGAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCCGTGACATCT 115	
Qy	415	SerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleTyrPro 434	

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RESULT 10
AAK14426/c
IDW AAK1444
XX AAK144
XX DF NOV
XX Human;
KW Human;
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                           Sequence 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4;
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                                                              LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSer
                                          CTGACCTCATTAGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCCTGGAGCTCCTGTCG
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04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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cancer; leukaemia; lymphoma;
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The present inver probes which are

invention

ntion provides a number of single exon nucleic acid derived from genomic sequences expressed in the human

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Percent Similarity:
Best Local Similarit
Query Match:
DB:
RESULT 12
AAI20932/
ID AAI2
XX AAI2
AC AAI2
XX Prob
XX WO20
PN WO20
PN 09-A
XX 30-J-J
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samples, which may enable the in
such as lymphoma, leukaemia and
the probes of the invention.
30-JAN-2001; 2001WO-US00670
                                                                             Probe
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                                                       uman; microarray; cancer; ss.
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Query Match:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 567 BP;
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                                 AspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThr
                                                                                                                                                                                                                                                                                                                  CTGACCTCATTAGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCGGAGCTCCTGTCG
                                                                                                                                                                                                                                                                                                                              LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSer
                                                                                                                                                                                                                       GATCCCGACGAGGTGGCCCGGCGCTGGGGAGAGCGGAAGAGCAAACCCCAACATGAACTAC
                                                                                                                                                                                                                                    AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr
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zing gene expression in
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2000US-0207456.
2000US-068408.
2000US-0632368.
2000US-0234687.
2000US-0234685.
2000US-0236359.
2000US-0236359.
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RESULT 13
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ID AA146176 s
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XX AA146176;
XX DE Probe #146
XX Probe; mic
KW Probe; mic
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XX The presen
CC The p
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Query Match
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon hucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 567
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                                                                                                                     {\tt AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr}
                                          GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG
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zing gene expression in huma
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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RESULT 14
AA106643/C
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XX AA1666
XX O9-OCT
XX Probe;
KW inflam
XX Homo s
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XX 29-JAN
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PR 30-IM
PR 30-IM
PR 31-SEP
PR 27-SEP
PR 27-SEP
PR 27-SEP
PR 21-SEP
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2000US-0207456.
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2000US-0236359.
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, breast. The probes are useful for predicting, diagnosing, grading,

nucleic acid probes. are useful for

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Novel single exon nucleic in a human breast:-

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pulmonary
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                   Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; pulmonary haemosiderosis; pulmonary haemosiderosis;
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Note: The sequence data for this patent did not form part of the printer.
                                                                                                                                          ABS14215;
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CC probes: Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a cc sample derived from human lung; comprising (a) contacting the array with a cc a collection of detectably labeled nucleic acids derived from human lung; measuring to comprising (a) contacting the array with a cc a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a cc a collection of detectably bound to each probe of cc in the array; identifying exons in a eukaryotic genome, comprising cof the eukaryote; and (b) detecting specific hybridisation of detectably collected an ucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method cc above and (b) measuring the expression of each probe is included tissues and/or cell types using hybridisation to a single exon cc microarray; having a probe with the exon, where a common pattern of cc expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (CCOPD), interstitial lung disease (ILD), familial idiopathic pulmonary disease. Pulmonary disease, Hermansky-Pudlak syndrome, fibrocystic pulmonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary candina frame of the invention.

CC hamonary alveolar proteinosis, Karagener syndrome, is a single exon con be open reading frame of the invention.
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21-SEP-2000;
27-SEP-2000;
                                                 probe open reading frame of the invention.
Note: The sequence data for this patent did not of the printed specification, but was obtained format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
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26-MAY-2000;
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hyaline membrane disease; open reading frame; ORF.
                                ftp.wipo.int/pub/published_pct_sequences
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435 AsnThrArgLeuProAlaAlaHisMetProSerHisLeuGlyThrTyrTyr 451	415 SerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleTyrPro 434	395 AlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThrSer 414	375 ProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHis 394 	355 GlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnProHis 374 	335 ASPLYSLeuSerArgAlaLeuArgTyrTyrTyrASpLysAsnIleMetThrLysValHis 354 	315 AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr 334 	295 AspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThr 314 	275 LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSer 294     :::	US-09-902-772-2 (1-451) x ABS14215 (1-567)	Alignment Scores:  2.91e-71  Pred. No.:  948.00  Matches:  169  Percent Similarity:  97.748  Best Local Similarity:  95.488  Mismatches:  4  Query Match:  38.798  Gaps:  0

Search completed: November 9, 2002, 17:14:26 Job time: 238.257 secs

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; TYPE: DNA
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Patent No. 6294354

GENERAL INFORMATION:

APPLICANT: Chugai Selyaku Kabushiki Kaisha, 5001, Iwamoto et

TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes

FILE REFERENCE: chugai selyaku Kabushiki kaisha 5001

CURRENT APPLICATION UNMBER: US/08/878,177

CURRENT FILING DATE: 1997-06-18

NUMBER OF SEQ ID NOS: 7
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Sequence 3, Application US/08878177

Patent No. 629434

GENERAL INFORMATION:

APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, 1

TITLE OF INVENTION: Cell Calcification Suppressing

TITLE OF INVENTION: the Proteins

FILE REFERENCE: chugai seiyaku kabushiki kaisha 500

CURRENT APPLICATION NUMBER: US/08/878,177

CURRENT FILING DATE: 1997-06-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

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Sequence 3, Application U
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Delattre,
APPLICANT: Delattre,
APPLICANT: Desmaze, C
APPLICANT: Melot, The
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Delattre, Olivier
Desmaze, Chantal
Melot, Thomas
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APPLICANT: Plougastel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Thomas, Gilles
APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANC
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM S
TITLE OF INVENTION: TRANSLACATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
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FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: PGIGGY CORNATION:
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MEDIUM TYPE: Floppy disk
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ZIP: 19102
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                            SerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisAlaHisPro
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CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application Patent No. 6268216 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for
TITLE OF INVENTION: Useful in the Treatment o
FILE REFERENCE: CASE-03828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Deneris, Evan S. APPLICANT: Fyodoro, Dmitry V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Rattus
FEATURE:
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Patent NO. 6384204
GENERRAL INFORMATION:
APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-04027
CURRENT APPLICATION NUMBER: US/09/435,335
CURRENT FILING DATE: 1999-01-05
EARLIER FILING DATE: 1999-07-26
RUMBER OF SEQ ID NOS: 23
GOVERNMENT DATE: DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1752
                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (112)..(1131)
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus
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	PUTER EDIUM OMPUTE PERATI	
	STREET: Two Penn Center, Suite 1800 CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A. ZIP: 19102	
ENES	ENTION: OLIGONUCLEOTIDES TARGETING CO QUENCES: 55 CE ADDRESS:	
	INFORMATION: CANT: Calabret CANT: Skorski, OF INVENTION:	
	6 306-691B-43 306-691B-43 ence 43, Applica nt No. 5734039	g S S S S S
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444	ThrArgLeuPro	Qy
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911	852 CGCCGCTGCCGCCGCCAGCGGCAGCCGCCGCCAGGATGGCGCACTTTACAAGCTCCC	ф
384	376ProGluSerSerMetTyrLysTyrPr	Qy
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791	732 ACTGCGCTACTACTACGACAAAAACATCATGAGCAAGGTGCACGGCAAGCGGTACGCCTA	Db
360	340 aLeuArgTyrTyrTyrAspLysAsnIleMetThrLysValHisGlyLysArgTyrAlaTy	Qy
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Query Match:
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REFERENCE/DOCKET NUMBER: 8321-8
FELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEFX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1604 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
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CURRENT APPLICATION DATA:
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984 ATGTGCATGGGGAGGACCAGTCGTGGTAAACTCGGGGGCCCAGGACTCTTTTGAAAGCATA 1043
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TOPOLOGY: linear
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                                                      ACAGACACCTTGCAGAATGACTACTTTGCTATCAAACAAGAAGTCGTCACCCCAGACAAC
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                         -----ThrThrArgProAspLeuProTyrGluGlnAlaArgArgSer--- 231
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ATTORNEY/AGENT INFORMATION:  NAME: DiGiglio, Frank S.  REGISTRATION NUMBER: 31,346  REFERENCE/DOCKET NUMBER: 8586  TELECOMMUNICATION INFORMATION:  TELEPHONE: 516-742-4343  TELEFAX: 516-742-4345  TELEFAX: 516-742-4365  TELESTA: 230 901 SANS UR FORMATION FOR SEQ ID NO: 9:  SEQUENCE CHARACTERISTICS:  LENGTH: 1604 base pairs  TYPE: nucleic acid	COUNTRY: USA ZII: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/06251 FILING DATE: 1930630 CIASSITETCATTON:	T 7  S93-06251-9  uence 9, Application PC/TUS9306251  NERAL INFORMATION: APPLICANT: Wickstrom, Eric and Rife, Jason P. TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates CORRESPONDENCE: 93  CORRESPONDENCE ADDRESS: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: NY	AspPheHisGlyIleAlaGlnAlaLeuGlnProHisProProGlu 377 	TyrTyrAspLysAsnIleMetThrLysValHisGlyLysArgTyrAlaTyrLysPhe 362                  :::	GlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAlaLeuArgTyr 343    :::     :::        GAAAGAGGAAAACATAAGATGAATTATGAGAAACTGAGCCGTGGCCTACGCTAC 1463	TrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAlaArgArgTrp 323	GlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAsnCysIleThr 303 	ProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGlnIle 283 ::: ::      ::::::	GlnArgProGlnLeuAsp 263          :: CCCAACCACAAGCCCAAGGGCACCTTCAAGGACTATGTGCGGGACCGTGCTGACCTCAAT 1223	ThrValProLys257 ::::: :: :: ::	AlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSer 250 ::::::

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                                          AAGGACAAGCCTGTCATTCCTGCTGCTGCCCTAGCTGGCTACACAGGCAGTGGACCAATC
                                                                                               CCCAACCACAAGCCCCAAGGGCACCTTCAAGGACTATGTGCGGGACCGTGCTGACCTCAAT
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                                                                    ProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGlnIle
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Query Match:
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; LOCATION: (291)..(1700)
US-09-344-579-1
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APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/344,579
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
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TYPE: DNA
ORGANISM: HOMO
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                                                             GENERAL INFORMATION:
APPLICANT: Mavroth
APPLICANT: Blair,
APPLICANT: Fisher,
APPLICANT: Beal Jr
                                                                                                                                           Sequence 1, Application US/08469412A Patent No. 5856125
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APPLICANT: Fisher, Robert J. APPLICANT: Beal Jr., Gregory J. APPLICANT: Athanasiou, Meropi A. APPLICANT: Squaras, Dionyssios N. TITLE OF INVENTION: The ERF Genet NUMBER OF SEQUENCES: 16
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Blair, Donald G.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-902-772-2 (1-451) x US-08-469-412A-1 (1-2667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2667 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/469
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowsk1, Euge
REGISTRATION NUMBER: 37,330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTED
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LOCATION: 123..1769
OTHER INFORMATION: /r
OTHER INFORMATION: Fa
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CITY: San Francisco
STATE: California
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STRANDEDNESS: single
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                                                GCCGGGCCCTGCGCTATTACTATAACAAGCGCATTCTGCACAAGACCAAGGGGAAACGGT
                                                                            erArgAlaLeuArgTyrTyrTyrAspLysAsnIleMetThrLysValHisGlyLysArgT
                                                                                                           AGGTGGCCCGGCTGTGGGGCGTTCGCAAGTGCAAGCCCCAGATGAATTACGACAAGCTGA
                                                                                                                                                                          ACCAGGGCGTCATTGCCTGGCAGGGGGACTACGGGGAATTCGTCATCAAAGACCCTGATG
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40.78%
14.01%
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Factor) cDNA"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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318 306 246

186 298 133 278

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Pred. No.:
Score:
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   Percent Similarity:
                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-Feb-1998
FILING DATE: 10-Feb-1998
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                           NAME/KEY: CDS
LOCATION: 123..170
OTHER INFORMATION:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Garrett-Wackowski, Eugenia
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                                                                                                                                                                                                                                                   Sequence 1, Application US/08875944B Patent No. 6096542
                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FUJINAGA, Kei
APPLICANT: YOSHIDA, Koichi
APPLICANT: HIGASHINO, Fumihiro
TITLE OF INVENTION: CANCER CONTROL
NUMBER OF SEQUENCES: 5
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                       STREET: 624 Nintl
CITY: Washington
STATE: D.C.
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                                                                                          COUNTRY:
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                                                                                                                                               ADDRESSEE:
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APPLICATION DATA:
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                                                                                           USA
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Indels:
               Version #1.30
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGTH: 2064 base pairs
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FILING DATE: 09-CAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FUJINAGA=1
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: JP 07-020173
FILING DATE: 08-FEB-1995
PRIOR APPLICATION DATA:
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                              200 AlaThrPheIlePhePro-----AsnThrSer------ValTyrProGluAla 213
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                                                           GCCATGGGTACCTCGGGG-----
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(202) 737-3528
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ũ	SULT 12 -09-116-049-3 -09-116-049-3 Sequence 3, Application US/09116049A Sequence 3, Application US/09116049A PARTICANT: HUNG, Men-Chie APPLICANT: HUNG, Men-Chie TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS FILE REFERENCE: UTSC:582 CURRENT APPLICATION NUMBER: US/09/116,049A CURRENT FILING DATE: 1998-07-15 NUMBER OF SEQ ID NOS: 11 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver: 2.0	RESULT US-09- US-09- ; Sequ ; Pate ; Pate ; GENE ; GENE ; TIT ; TIT ; FIL ; CUR ; CUR ; NUM	
	1398 GGCTGTTCCCCCTGCC 1413	Db	
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, ,	398 nLysMetAsnPheValAlaProHisProProAlaLeuProValThrSerSerSerPhePh :::	P Q	
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383	roGluSerSerMetTyrLysTy	Qy	
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778	719 AACAGACGGACTTCGCCTACGACTCAGATGTCACCGGGTGCGCATCAATGTACCTCCACA	В	
257	sProThrGlnSerLysAlaThrGlnProSerSerThrValProLysThrGluAsp	Qy	
718	659 TGGACCAGGGTGGGGTCAATGGGCACAGGTACCCAGGGGCGGGGGGGG	В	
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   273 SerArgLeuAlaAsnProGly----
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                                                                                     CAGAGGGCTTCTCTGGGCCCTCTCCAGGTGACGGGGCCATGGGCTATGGCTATGAGAAAC
                                                                                                                                            AACAGACGGACTTCGCCTACGACTCAGATGTCACCGGGTGCGCATCAATGTACCTCCACA
                                                                                                                                                                         HisProThrGlnSerLysAlaThrGlnProSerSerSerThrValProLysThrGluAsp 257
                                                                                                                                                                                                       TGGACCAGGGTGGGGCAATGGGCACAGGTACCCAGGGGCGGGGGTGGTGATCAAACAGG
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                            CTCTGCGACCATTCCCAGATGATGTCTGCGTTGTCCCTGAGAAATTTGAAGGAGACATCA
                                                                                                                GlnArgProGlnLeuAspProTyrGlnIleLeuGlyPro-------
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SEQUENCE	9 11 12	REG REF	ATTORNE :	APP	SOF	COM	MEDIUM TYPE: F	ZIP:	COU	CITY:	ADD	NUMBER OF	APPLICANT:	APPLICANT: Hung,	Patent No.	13 780-	1398	436	1345	418	1285	398	1225	383	1195	364	1138	344	1078	324	1018	304	958	284	899
	TELEPHONE: TELEFAX: RMATION FO	REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER:	ATTORNEY/AGENT INFORMATION: NAME: Wilson, Mark B.	APPLICATION NUMBER: FILING DATE: 10-JA	SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:	COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS	IUM T	77	Υ	• • •	ADDRESSEE: ARNOLD,	ROF	OF I	CANT:	ب ؛	35	GGCTGTTCCCCCTGCC		GGCCCGCCCAG-CCATTT-	eAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleTyr	GAGGACACAGTCCCTTTGTCCCACTTGGATGAGAGCCCCGCCTACCTCCCAGAGCTGGCT	nLysMetAsnPheValAlaProHisProProAlaLeuProValThrSerSerSerPhePh	GCCTT	rProSerAspLeuProTyrMetSerSerTyrHisAlaHisProGl		PheHisGlyIleAlaGlnAla-LeuGlnProHisProProGluSerSerMetTyrLysTy	TATTATGAGAAAGGCATCATGCAGAAGGTGGCTGGTGAGCGTTACGTGTACAAGTTT	ТУГТУ	GCATCCAGAAGAACCGGCCAGCCATGAATTACGACAAGCTGAGCCGCTCGCT	GlyGl	TGGACGGCCGGGGAATGGAGTTCAAGCTCATTGAGCCTGAGGAGGTCGCCAGGCTCTGG	TrpGl		GlnLe	
CHARACTERISTICS:	(51) FOR SI	E/DOCI	AGENT I	ATE:	PLICA:	G SYS	YPE:	7210-4433	Texas	Houston	E: CE	SEQUENCES	OF INVENTION: PEA3 1	Hung,	5922688	1	TTCCC	euPro	ceccc	laPro	CACAG	etAsn	cccee	er		sGlyI	TGAGA	rAspL	CCAGA	uArgL	GGGCC	uGlyT	GTGGC	uTrpG	 GAAGG
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Query Match:
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                                                                              Alignment Scores:
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                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,268
FILING DATE: 30-Apr-1999
CLASSIFICATION: <UGNnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,835
FILING DATE: 10-CAN-1997
ATTORNEY/ACENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UTSC500
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MEDIUM TYPE: Floppy disk
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                                                                                                                              SEQUENCE DESCRIPTION: SEQ
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                    LeuSerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLys 312
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RESULT 15 US-09-116-049-1 Sequence 1, Application US/0911; Patent No. 6248351; GENERAL INFORMATION: APPLICANT: Hung, Men-Chie; TITLE OF INVENTION: HUMAN PEA: FILE REFERENCE: UTSC:582; CURRENT APPLICATION NUMBER: US: CURRENT FILING DATE: 1998-07-1; NUMBER OF SEQ ID NOS: 11 SOFTWARRE: PATENTIN Ver. 2.0 ; SEQ ID NO 1 LENGTH: 2410
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:
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	ValHisGlyLysArgTyrAlaTyrLysPhe 362	353	γ Q
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1508	CTAATTGAACCTGAAGAGTTGCCAGGCTCTGGGGTATCCAGAAGAACCGGCCAGCCA	1449	В
332		313	Qy
1448	CTGGATGACCCCAACAATGCTCATTTCATTGCTTGGACAGGCCGGGGAATGGAGTTTAAA	1389	В
312	LeuSerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLys	293	VΩ
1388	AG-GGGCCACCCTACCAGCGCCGGGGTGCCTTACAACTGTGGCAGTTTCTGGTGGCCCTG	1330	Вb
292		278	Qγ
1329	GCATTGTCCCTAAAAAATTTGAAGGAGACATCAAGCAGGAAGGGATTGGAGCTTTCCGGG	1270	뭥
277		268	Qy
1269	GTGATGGAGTGATGGGTTATGGCTATGAAAAATCCCCTTCGACCATTCCCAGATGATGTCT	1210	망
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1209	ATGTCCCTGGATGTGCATCAATGTACCTCCACCCAGAGGGCTTCTCTGGACCCTCTCCAG	1150	Ъ
266		247	Qγ
1149	GGTACCCAGGGGGGGGGGGGGTGATCAAACAGGAGCGCACAGACTTCGCCTACGACTCAG	1090	B
246	TrpThrSerHisSerHisProThrGlnSerLysAlaThrGln	233	Qy
1089	CCCTGTACGAACAGGCTGGCCAGCCCGCTTCAAGCCAGGGTGGGGTCAGTGGGCACA 1089	1033	뮹
232	IleThrThrArgProAspLeuProTyrGluGlnAlaArgArgSerAla	217	Qy
1032	AACTGTCGGAGCCCTGCCCACCCTACCCCCAGCAGAACTTCAAGCAGGAGTACCATGACC	973	B
216	SerValTyrProGluAlaThrGlnArg	208	Qy
972	CATCTCCTCAGGGAGGGGGCCGGGAACCTCTCCCAGCCCCCTATCAACACC 972	922	В

Search completed: November 9, 2002, 19:48:56 Job time: 69.9451 secs

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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US/09864761  K.  GENOME-DERIVED SINGLE EXON NUCLEIC EXPRESSION ANALYSIS BY MICROARRAY US/09/864,761 US/09/864,761 US/09/864,761	ALIGNMENTS	09-920-300A-1	US-09-864-761-27055	US-09-777-564-468	US-09-822-827-44	US-09-030-606-44	US-09-780-669-44	US-09-925-301-207	US-09-922-217-1105	US-09-880-10/-3420 US-09-967-768A-192	US-09-964-824A-563	US-09-964-824A-101	US-UY-841-963A-3	US-09-925-297-309	US-09-764-864-320	US-09-841-963A-1	US-09-925-297-257	US-09-140-9435-1	US-10-033-528-1788	US-09-880-107-3316	US-10-108-605-128	US-10-108-605-124	US-09-864-761-12798	US-09-864-761-5035	US-09-864-761-20364	US-09-864-761-7427	US-09-925-300-420	118-10-033-528-1693	-10-033-528- <b>171</b> 6	-09-920-300A-17	US-U9-864-/61-1653	00 00 10 10 10 10 10 10 10 10 10 10 10 1
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: US 09/608,408

FILING DATE: 2000-06-30

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FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00670
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FILING DATE:
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FILING DATE: 2001-01-30
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|GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG
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                                              GATAAGCTCAGCCGCCCCCCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCAT
                                                             AspLysLeuSerArgAlaLeuArgTyrTyrAspLysAsnIleMetThrLysValHis
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NN: EXPRESSED IN PLACENTA, SIGNAL = 1.4

NN: EXPRESSED IN HELLOO, SIGNAL = 1.7

NN: EXPRESSED IN HELLA, SIGNAL = 1.7

NN: EXPRESSED IN HEART, SIGNAL = 0.92

NN: EXPRESSED IN LUNG, SIGNAL = 1.8

NN: EXPRESSED IN HEART, SIGNAL = 1.8

NN: EXPRESSED IN HARAIN, SIGNAL = 1.5

NN: EXPRESSED IN BAULT LIVER, SIGNAL = 1.5

NN: EXPRESSED IN HEATA, SIGNAL = 1.5

NN: EXPRESSED IN HEATA, SIGNAL = 1.9

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

NN: SWISSPROT HIT: P11308, EVALUE 9.00e-90

NN: NT HIT: M17254.1, EVALUE 0.00e+00

NN: NT HIT: M17254.1, EVALUE 0.00e+00
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948.00
97.74%
95.48%
38.79%
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: Annom:
SEQ ID NO 20472
LENGTH: 473
TYPE: DNA
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APPLICANT: Hank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXP
FILE REFERENCE: Acomica-X-1
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                              NUMBER
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
APPLICATION NUMBER: PCT/US01/00666
                                                              FILING DATE: 2001-01-
R OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT/US01/00669
APPLICATION 2001-01-30
TTT-ING DATE: 2001-01-07
TTT-ING DATE: 2001-01-665
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APPLICATION NUMBER: PCT/US01/00664
APPLICATION NUMBER: PCT/US01/00666
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FILING DATE: 2000-08-03
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APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                                               Sequence
                                                                                                                  NUMBER.
2000-09-21
US 09/608,4
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, David K.
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                                               Listing
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DB:
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                                                    GENERAL INFORMATION:
APPLICANT: Eyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC
FILE REFERENCE: 210121.553
                                                                                                                                                 Sequence 54, Application US/09923779 Patent No. US20020076721A1
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
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**HER INFORMATION: EXPRESSED IN BIA14, SIGNAL = 1.2

**HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

**HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

**HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97

**HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97

**HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

**HER INFORMATION: EXPRESSED IN HEALTA, SIGNAL = 1.4

**HER INFORMATION: EXPRESSED IN HEALT, SIGNAL = 1.4

**HER INFORMATION: EXPRESSED IN HEALT, SIGNAL = 1.4

**HER INFORMATION: SET_HUMAN HIT: P11308, EVALUE 0.00e+00

**HER INFORMATION: SWISSPROT HIT: P11308, EVALUE 6.00e-88

**HER INFORMATION: NT HIT: M17254.1, EVALUE 0.00e+00
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Mismatches:
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Gaps:
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 356, 363, 417, 4
; LOCATION: 537, 545
; OTHER INFORMATION: n = A,T
US-09-923-779-54
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Query Match:
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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LENGTH:
                                                                                                                                                                                                                                                         Sequence 3705, Application Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                          APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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US-09-864-761-3705
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
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FILING DATE:
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FILING DATE: 2000-66-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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FILING DATE: 2001-01-30
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FILING DATE:
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            SerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleTyr 433
                                           HisalaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThr 413
                                                                                         HisGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuglnPro 373
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DULT LIVER, SIGNAL =

N FETAL LIVER, SIGNAL =

N BRAIN SIGNAL = 1.1

N BOAL SIGNAL = 1.2

N BOAL MARROW, SIGNAL = 0

N PLACENTA, SIGNAL = 1.4
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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OR APPLICATION NUMBER: PCT/USO1/00666

FILING DATE: 2001-01-30

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FILING DATE: 2001-01-30

FOR PILING DATE: 2001-01-30

FOR APPLICATION NUMBER: PCT/USO1/00669

FOR APPLICATION NUMBER: PCT/USO1/00669

FOR PILING DATE: 2001-01-30

FOR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00665

FOR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00665

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OR APPLICATION NUMBER: PCT/USO1/00668
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00662
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Chen, Wensheng
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ESSED IN HELLOO, SIGNAL = 1.7
ESSED IN HELA, SIGNAL = 1.7
ESSED IN HEART, SIGNAL = 0.92
ESSED IN BONE MARROW, SIGNAL = 1.8
ESSED IN LUNG, SIGNAL = 1.8
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US-09-864-761-1653

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Percent Similarity:
Best Local Similarity:
Query Match:
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                             US-09-902-772-2 (1-451) x US-09-850-799-1 (1-1752)
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Best Local Similarity:
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CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/360,779
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1752
TYPE: DNA
ORGANISM: Rattus norvegicus
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APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Tinothy J.
APPLICANT: Hendricks, Tinothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-03828
                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (112)..(1131)
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ULT 7 09-920-300A-1716 09-920-300A-1716 equence 1716, Application US/09920300A atent No. US20020136728A1 ENERAL INFORMATION: EAPPLICANT: King, Gordon E. APPLICANT: Weagher, Madeleine Joy APPLICANT: Xu, Jiangchun APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547 CURRENT APPLICATION NUMBER: US/09/920,300A CURRENT FILING DATE: 2001-07-31	4 oSerHisLeuGlyThrTyrTyr 451            ::    7 TTCGCACTTGGGGGGTCATTAT 1128	1 yIleTyrProAsnThrArgLeuProAlaAlaHisMetPr 	9 aAlaProAsnProTyrTrpAsnSerPro	9 sMetAsnPheValAlaProHisProProAlaLeuProValThrSerSerSerPhePheAl  :::	GGCTGGTCTGGCTCCACTGCCCTTCCCCGGCCTC	d oSerAspLeuProTyrMetSerSerTyrHisAlaHisProGlnLy	CGCCGCTGCCGCCGCCGCAGCCGCCAGCCCCCAGGATGGCGCACTTTACAAGCTCC	ProGluSerSerMetTvrLvsTvrP	TLYSPHEASPPHEHISGIYILEALAGIHAIALEUGHPPFHISPFO	ACTGCGCTACTACGACAAAAAACATCATGAGCAAGGTGCACGGCAAGCGCTACGC	aLeuArgTyrTyrTyrAspLysAsnIleMet	0 aArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAl 	CTGCATCGCGTGGGAGGGCGACGGCCACGGCGAGTTCAAGCTCACCGACCCCGACGAGGTGGC	CGGGCAGATCCAGTTGTGGCAGTTTCTACTGGAGCTGCTGGCAGACCGCGCGAACGCC	rGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeu	GAGCTGGGGGCCGGGCAGCCCTGCGGTACAGAAA	: <u>G</u>	3 GATCAACATGTACCTACCAGATCCCGTCGGAGATGGTCTTTTAAGGAAGG	SerSerThrValProLysThrGluAspGl	BGTCCCGGCAGCGATGAGACAGAGCGGCACCTCCCAGCCCCTGCT	9 ArgArgSerAlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSer	
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1716
LENGTH: 2188
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us-o Qy Db Qy Qy Db	Alignmer Pred. No Score: Percent Best Loc Query Ma DB:	RESULT US-10-1 Pates Pat	Оy	Qу	Qy Db	dp Qy	Оy	P 64	dd VO
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-772-2 (1-451) x US-10-033-528-1716 (1-2188)	nment Scores: 4.21e-35 Length: 4.44.50 Matches: ent Similarity: 41.288 Conservative: Local Similarity: 30.718 Local Similarity: 31.718 Indels: y Match: 12 Gaps:	28-1716 1716, Application US/10033528 . US20020131971A1 NFORMATION: T: King, Gordon E. T: Kneagher, Madeleine Joy T: Xu, Jiangchun T: Secrist, Heather INVENTION: COMPOSITIONS AND METHODS FOR INVENTION: AND DIAGNOSIS OF COLON CANCE TRENCE: 210121.547C1 INVENTION NUMBER: US/10/033,528 APPLICATION NUMBER: US/10/033,528 FILING DATE: 2001-12-26 F SEQ ID NOS: 1896 F SEQ ID NOS: 1896 F SEQ TO NOSE 1896 S: FastSEQ for Windows Version 4.0 1716 1716 NA M: Homo sapiens	salaHisProGlnLysMet 400            ::::::   AGCCCATCCTGACCAGCTG 1690	oProGluSerSerMetTyrLysTyrProSerAspLeuPro ::: GGAGGACTGAGGTCGCCGGGACCACCCTGAGCCGGCCCCAGG	AspPheHisGlyIleAlaGl :::	) nIlemetThTLysValHisGlyLysArgTyrAlaTyrLysPhe	ILYSPIOASNMETASNTYIASPLYSLEUSEIAIGALALEUAIGTYITYITYIASPLYSAS 		eLeuLeuGluLeuLeuSerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAs 
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                               AGCCCATCCTGACCAGCTG
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                                                                                                                                  oProGluSerSerMetTyrLysTyrProSerAspLeuPro---TyrMetSerSerTyrHi
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CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1693

LENGTH: 2268
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APPLICANT: Meagher, Maddeline Joy
APPLICANT: Weagher, Maddeline Joy
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND JAGNOSIS OF COLON CANCER
                                          1096 AATTCTGGGACTCCCAAAGACCACGACTCCCCTGAGAACGGTGCGGACAGCTTCGAGAGC
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GENERAL INC.

APPLICANT: King, Gordon E.

APPLICANT: Weagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1693
LENCTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-1693
                                                Percent Similarity:
Best Local Similarity:
Query Match:
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1634	CATCATCCACAAGACGTC	1575	Db
362	nIleMetThrLysValHisGlyLysArgTyrAlaTyrLys	348	δÃ
1574	TANGCCCANGATGAACTACGAGAAGCTGAGCCGGGGCTTACGCTACTATTACGACAAGAA	1515	Db
348	rLysProAsnMetAsnTyrAspLysLeuSerArgAlaLeuArgTyrTyrTyrAspLys	328	Qγ
1514	ATGGGAGTTTAAGCTCGCCGACCCCGATGAGGTGGCCCGGCCGG	1455	В
328	luPheLysMet	308	Qy
1454	TCTCCTGGAGCTGCTATCAGACAAATCCTGCCAGTCATTCAT	1395	ДЬ
308	eLeuLeuGluLeuSerAspSerSerAsnSerAsnCysIleThrTrp	288	Qy
1394	TATACCTGCAGCTGTGCTGGCCGGCTTC	1335	Db
288	GlySerGlyGlnIleGlnLeuTrpGlnP	279	Qy
1334	ATGTCTTTCAAGGATTACATCCAAGAGAGG-AGTGACCCAGTGGAGCAAGGCAAACC	1276	DЬ
278	ThrSerSerArgLeuAlaAsnPr	271	Qy
1275	CCTTCCTTCGAGAGCTTCGAAGATGACTGCAGCCAGTCTCTCTGCCTCAATAAGCCAACC	1216	DЬ
270		270	Qy
1215	Ä.	1156	DЬ
270	pGlnArgProGlnLeuAspProTyrGlnIleLeuGlyPr	257	Qy
1155	AATTCTGG	1096	망
257		252	Qy
1095	:  -    GTCACCTACTGCTCTGTCAGTCAGGACTTCCCCAGGCAGCAACTTGAATTTGCTCACCAAC	1036	Ъ
251	rSe	249	Qy
1035	GTACTCAGCTCTGAGCAGGAGTTTCAGATGTTCCCCAAGTCTCGGCTCAGCTCCGTCAG	976	Дb
249	rGlnSerLysAlaThrGln	240	Qy
975	ACACAGAATTACCCCAAAGGCGGCCTCCTGGACAGCATGTGTC	916	뮻
240	aArgArgHisSerHisPr	228	Qy
915	CATTGGATTAACAGCAATACATTAGGTTTTGGCAC	856	Ъ
228	AspLeuProTyr-C	222	Qy
855	GAAAAGACAGAAGATCAATATGAAGAAAATTCACACCTCACCTCC	805	В
221	PheIlePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgPr	202	Qy
804	GACTITGTGGGTGACATTCTCTGGGAACATCTGGAGCAAATGATCAAAGAAAACCAA	748	Ъ
201	SerTyrAsnAlaAsp	182	Qy
747	GGCATGAATGGCCAGATGCTGTGTAACCTTGGCAAGGAACGCTTTCTGGAGCTGGCACCT	688	рь
181	AsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThrPro	162	Qy
687		631	DЬ
161	TrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspI	142	Qy
630	::      :::	571	В
141	GluargargValIleValProAlaaspProThrLeuTrpSerThraspHisValArgG	122	Qy

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IENGTH: 1884

TYPE: DNA
ORGANISM: HOMO SapienS
FEATURE:
NAME/KEY: misc feature
LOCATION: (55)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
INCOTION: (283)
COTHER INFORMATION: n equals a,t,g, or OTHER INFORMATION: n equals a,t,g, or US-09-925-300-420
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US-09-925-300-420
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VEI. 2.0
SEQ ID NO 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
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OTHER INFORMATION: EXPRESSED IN PLACEN.
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OTHER INFORMATION: EXPRESSED IN LUNG, OTHER INFORMATION: EXPRESSED IN ADULT IOTHER INFORMATION: EXPRESSED IN HEATION
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SEQ ID NO 7427
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APPLICATION NUMBER: PCT/US01/00661
TILING DATE: 2001-01-30
TILING DATE: 2001-01-00670
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PRICING DATE: 2001-01-
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: US 0
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FILING DATE: 2001-01-30
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ED IN BONE MARROW, SIGNAL = 2.1
ED IN LUNG, SIGNAL = 1.3
ED IN ADULT LIVER, SIGNAL = 0.76
ED IN HEART, SIGNAL = 2.1
ED IN FETAL LIVER, SIGNAL = 2.1
ED IN FETAL LIVER, SIGNAL = 2.1
ED IN BRAIN, SIGNAL = 2.1
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OTHER INFORMATION: MAP TO APO00021.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: NT HIT: M21535.1, EVALUE 1.00e-113
OTHER INFORMATION: SUISSPROT HIT: P11308, EVALUE 3.00e-37
US-09-864-761-21761
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB ;
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
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NUMBER OF SEQ ID NOS: 49117
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Hanzel, David K.
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PRIOR FILING DATE: 2000-05-26
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APPLICANT: Penn, Shairon G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

ITITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-x-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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EXPRESSED IN BONE MARROW, SIGNAL = 0.73

EXPRESSED IN ADULT LIVER, SIGNAL = 0.52

EXPRESSED IN FETAL LIVER, SIGNAL = 0.55

EXPRESSED IN FETAL LIVER, SIGNAL = 0.55

SWISSPROT HIT: P11308, EVALUE 4.00e-38

NT HIT: M21535.1, EVALUE 1.00e-113

EST_HUMAN HIT: AW948986.1, EVALUE 1.00e-108
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 5035
LENGTH: 477
TYPE: DNA
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; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = US-09-864-761-5035
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OR APPLICATION NUMBER: PCT/US01/00665
IOR FILING DATE: 2001-01-30
IOR APPLICATION NUMBER: PCT/US01/00668
IOR APPLICATION NUMBER: PCT/US01/00663
IOR APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Database: EST:*  1: em_estba:*  2: em_esthum:*  3: em_estin:*  4: em_estmu:*  5: em_estov:*  6: em_estpl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

REFERENCE AUTHORS TITLE	VERSION VERSION SEYWORDS SOURCE ORGANISM	RESULT 1 AJ456498 LOCUS DEFINITION		U T	43 59	n 01	э •	38 61	, 00	5 4	ωι	91	0 4	8 72	26 27	5 77	3 79	2 1 8 1	0 4		6 93	5 4	- ω	1 2 97	97			TOC	101	2	Result No. Sco
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s; Phasiani	; Vertebrata; Euteleostomi;	A linear EST·22-APR-2002 ne 8m13r2, mRNA sequence.		AA467723 ve02h06.r AJ456869 AJ456869	AL598619 DKFZp313I		BQ215477 AGENCOURT	AJ445352 AJ445352 AJ446143 AJ446143		BE831331 QV4-MT004	BQ062565 AGENCOURT		UN BE	АМ421310 fj89906. у	34	BF566705 UI-R-BJ0р AJ456506 AJ456506	BB656030 BB656030	AL554108 AL554108	BG3905/2 602416344 BG256864 602371114	BI558530 603240526	BG259459 602378556 BB577887 BB577887	BB639043 BB639043 BM489636 pqm2n.pk0	BQ953977 AGENCOURT	AU136709 AU136709 AW948986 OV4-FT000	BM088063 501436 MA BG390291 602416255	BB660034 BB660034	558012	BQ212127 AGENCOURT BG388025 602412867	233264 AC	AJ456498 AJ456498 BM456833 AGENCOURT	Description

	Gallus gallus bursal lymphocyte EST	TITLE
	Buerstedde, J.M.	AUTHORS
	1 (bases 1 to 827)	REFERENCE
	Phasianinae; Gallus.	
formes; Phasianidae;	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
ta; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Gallus gallus	ORGANISM
	chicken.	SOURCE
	EST.	KEYWORDS
	AJ456498.1 GI:20266594	VERSION .
	AJ456498	ACCESSION
lone 8m13r2, mRNA sequence.	AJ456498 riken1 Gallus gallus cDNA clone 8m13r2, mRNA sequence.	DEFINITION
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                  GluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeu
                                                                                                                  ProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSer
                                                                                                                                                                                                                                                                                                                    AGTAGCTCACTGCTCTAC---AATACTCCATCCCACACAGAAGCTTCCTCACGTCTT
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Contact: Buerstedd
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/clone_lib="riken1"
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/dev_stage="2-3 weeks old"
/note="CB inbred strain"
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GluAlaLeuSerValValSerGluAspGlnSerLeuPheGluCysAlaTyrGlySerPro

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GAAGCCTTATCAGTTGTGAGTGAGGACCAGTCGTTGTTTGAGTGTGCCTACGGAACGCCA
HisLeualaLysThrGluMetThralaSerSerSerGluTyrGlyGlnThrSerLys

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Plate: LLAM12347 row: f column: 10
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT_6404041
5', mRNA sequence.
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/clone_lib="NIH_MGC.92"
/clone_lib="NIH_MGC.92"
/lisue_type="mbbryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: No. Site_2: Sall; Cloned unidirectionally; oligo-dT prime: Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologi. Note: this is a NIH_MGC Library."
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                                                                    AGENCOURT_7565836 NIH_MGC_5', mRNA sequence.
BQ233264
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13279 row: h column: 07
High quality sequence stop: 608.
Location/Qualifiers
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Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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                                                                                                                                                                                                                                     /tissue_type="embryonal carcinoma, cell line"
/lab_host="DBH()B (phage-resistant)"
/note="organ: testis; vector: pCMV-SPORT6; Site_1: NotI.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
a 314 c 257 g 225 t 1 others
                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:6052136"
/clone_lib="NIH_MGC_92"
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                AACGAGCGCAGAGTTATCGTGCCAGCAGCATCCTACGCTATGGAGTACAGACCATGTGCGG
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Plate: LLAM10420 row: f column: 18
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Tissue Procurement: ATCC
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Contact: Robert St
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4521233"
/clone=lib="NHILMGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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CCTTCTTATGACTCTGTCAGGAGGAGGAGCATGGAACAATAATATGAACTCTGGCCTCAAC 175
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Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 949)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: LLAM11742 row: h column:
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                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Grow and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_GGAP_Mam4"
/tlssue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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 Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                Endocrine Pancreas Consortium Unpublished (2000) Other_ESTs: 1e01d08.x1
                                                                                  Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvill,R., Williams,T., Jackson,Y. and Bowers,Y.
                                    Contact: Douglas Melton, Klaus H.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 642)
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Fax: 617-495-857
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
Washington University Genome Sequencing Center For informati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtaining a clone please cont
(hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 4
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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/clone_lib="HR85 islet"
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Unpublished (2001)
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BB660034
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URL:http://genome.gsc.riken.go.jp,
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
,M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
wagi, K., Yoneda, Y., Ishikawa, T., Gawa, K., Tanaka, T., Matsuura
,S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
hayashizaki, Y., Caraki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
hayashizaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared wi
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Arakawa, T., Carninci, P., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su,Y. and Hayashizaki,Y.
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Tel: 81-45-503-9222
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RIKEN full-length enriched, 13 days embo
cDNA clone D430027L04 5', mRNA sequence
                      /dev_stage="13 days embryo"
/lab_host="DH10B"
                                                                                                                        /db_xref="taxon:10090"
/clone="D430027L04"
    /note="Site_1:
                                                                                                   /clone_lib="RIKEN full-length
                                                                                                                                                             organism="Mus musculus"
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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8.04e-90 984.00 96.94% 93.37% 40.26%

Length:
Matches:
Conservative:
Mismatches:
Indels:

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Gaps:

1 MetAlaSerThrIleLysGluAlaLeuSerValValSerGluAspGlnSerLeuPheGlu GlnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThr GlnTrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuPhe AsnGluArgArgValIleValProAlaAspProThrLeuTrpSerThrAspHisValArg GlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProProAsnMetThrThr CysAlaTyrGlySerProHisLeuAlaLysThrGluMetThrAlaSerSerSerSerGlu TyrGlyGlnThrSerLysMetSerProArgValProGlnGlnAspTrpLeuSerGlnPro ATGGCCAGCACTATTAAGGAGGCCTTGTCAGTTGTGAGCGAGGACCAGTCACTATTTGAG CAGAATATCGATGGGAAGGAGCTGTGCAAGATGACAAAGGATGACTTCCAGCGGCTCACG CAGTGGCTGGAGTGGAAAGAATATGGCCTNCTCGATGTGGACGTCTTACTATTT AATGAGCGCAGAGTGATCGTCCCTGCAGATCCTACTCTGTGGAGCACAGACCATGTCCGA GGGATGAGCTACGGCAGCTACATGGAGGAGGAGCATGTGCCGCCTCCCAATATGACCACA TCACCTGATGAGTGCAGTGTGAACAAAGGTGGGGAAGATGGTGGGCAGCCCGGATACTGTG SerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnVal TGTGCCTACGGAACGCCACACCTGGCTAAGACAGAGATGACCGCATCCTCTTCCAGTGAC 120 100 180 60 40 619 140 499 439 379 319 80 259

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1 (bases 1 to 592)

Smith, T. P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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PO Box 166, Clay Center, NE 68933-0166, USA
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Contact: Smith TPL
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Fax: 402 762 4390
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/db_xref="taxon:9913"
/clone_lb="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal. and endometrium."
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                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10429 row: m column: 13
High quality sequence stop: 820.
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602416255F1 NIH_MGC_92 Homo
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BG390291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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Location/Qualifiers
                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4524852"
/clone=lib="NH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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Primates;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                         CAGTGGCTGGAGTGGGCGTGAAAGAATATGGCCTTCCAGACGTCAACATCTTGTTATTC
                                                                                 AACGAGCGCAGAGTTATCGTGCCAGCAGATCCTACGCTATGGAGTACAGACCATGTGCGG
                                                                                                                                                                                                                                             TATGGACAGACTTCCAAGATGAGCCCACGCGTCCCTCAGCAGGATTGGCTGTCTCAACCC
                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
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/db_xref="taxon:9606"
/clone="PLACE1004911"
/clone="blaCE1004911"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-FT0005-110
500-201-f02at3=2000-05-11&t4=1)
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Shotgun sequencing of the human transcriptome with ORF expressed
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed low stringency conditions."
173 c 171 g 119 t
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/clone_lib="FT0005"
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IMAGE:6198592 5',
BQ953977
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                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
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/lab_host="DH10B"
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URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,

.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.
             Y. and Hayashizaki, Y.
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (20)
"""" 'Shinagawa, H., Kondo, S., Saito, T., Shinagawa, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kou
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nonura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasa
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                         sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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T., Shinagawa, A., A
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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thymus"
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ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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Townsend Hall, Newark, DE 19717,
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and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
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/db_xref="taxon:9031"
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,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host-"E. coli EMDH10B"
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/strain="Commercial broil
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### ALIGNMENTS

AAY01521 standard; Protein; 478 ₽

# AAY01521;

14-JUN-1999 (first entry)

# Chicken c-erg protein.

Chicken; C-11 protein; cell calcification inhibiting activity; cell calcification inhibiting agent; c-erg protein; arthritis deformans; ossification; spinal column ligament.

### Gallus gp.

JP11075871-A.

# 23-MAR-1999.

20-JUN-1997; 18-JUN-1997; 29-MAY-1998; 97US-0050297 97US-0878177 98JP-0166076

# (CHUS ) CHUGAI PHARM CO LTD (UYPE-) UNIV PENNSYLVANIA.

# WPI; 1999-257708/22. N-PSDB; AAX26552.

An active protein for inhibiting cell calcification - useful for measuring the calcification of a cell, for diagnosing arthritis

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      20-JUN-1997;
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                                                                              23-MAR-1999
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 PNTRLPAAHMPSHLGTYY
               PNTRLPAAHMPSHLGTYY
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                                                                                                               YDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein for inhibiting cell calcification the calcification of a cell, for diagnosing or ossification of spinal column ligament
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The invention relates to an Erg (a member of the Ets family of C transcription factors) modulator for use in medicine, where the modulator is not tumour necrosis factor-alpha (TNF-alpha) or interleukin-1 (IL-1). CC Also included are a method of screening for a drug or drug candidate, the offect of Erg on secreted protein, acidic, cysteine-rich convolving determining whether or not a group being screened modulates the effect of Erg on secreted protein, acidic, cysteine-rich (Osteonectin/BM-40) (SPARC), thrombospondin (TSP), rho-A (a Ras cysteined factor (VWF) RNA or polypeptide expression, or cysteined factor (VWF) RNA or polypeptide expression, or cysteined factor (VWF) RNA or a heterologous polypeptide that is under the control of one or more regulatory sequences of the SPARC, cysteined modulates the expression of Erg RNA in a given expression system, determining whether or not a group being screened modulates the expression of Erg RNA in a given cyste, determining whether or not a group being screened cystem, determining whether or not a proper sing an Erg binding of Erg to a nucleic acid comprising an Erg binding cyste, determining whether or not a nucleic acid hybridises with DNA of an cyste, determining whether or not a disorder such as a disorder in cystes acid knocks out or reduces expression of Erg. Erg based cystes acid comprising an Erg binding cystes acid comprising whether or not a cystes acid comprising whether or not a cystes acid cystes acid acid cystes ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 53-54; 75pp; English.
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82.9%;
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        9;
                                        Score 2180.5; DB 2
Pred. No. 2.4e-190;
            Mismatches
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    65;
Gaps
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primitive peripheral neuroectodermal tumour;
human chromosome 22; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosomal translocation; chimeric; chimaeric; Ewing sarcoma;
Ews gene; malignant melanoma; hum-fli-1; clone BM025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR44556 standard; Protein;
                                                                                                                                             Plougastel
                                                                                                                                                                    Aurias
                                                                                                                                                                                                           (CNRS )
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                                                                                                                                                                                                                                                                                                  19-MAY-1993;
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Zucman J;
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New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment

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RESULT 5
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Best Local S
Matches 291
                          02-OCT-2000; 2000WO-JP06840
                                                                                                                                                                                              Human; shear stress-response arteriosclerosis.
                                                                                                                                                                                                                                                            Human shear stress-response protein
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                                                                   12-APR-2001
                                                                                                             WO200125427-A1
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         AAB90792 standard;
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nilarity 57.7%;
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Pred. No. 1.7e-126;
5; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequences, proteins encoded by them and antibodies useful in diagnosis and treatment of vascular disease carteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                    GIYPN---TRLPAAHMPSHLGTYY 478
                                          LQPHPTESSMYKYPSDISYMPSQHAHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTS-TG
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                                                                                                                                                                                                                                                                                                             -PYRYNYKREY--DHMNGSRESPYDCSYSKCSKLYGGGESNPMNYNSYMDEKNGPPPPNM
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DB; AAH02915.
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Sekine S,
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Nakamura Y, Sugano
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57.5%; Pred. No. 6.9e-125;
Live 55; Mismatches 80;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical acoust of the collection of the content of the collection of the collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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27-SEP-2000;
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  NTRLPAAHMPSHLGTYY
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                                            PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                 DKLSRALRYYDKNIMTKV----
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
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RESULT 7
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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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04-OCT-2000;
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NTRLPAAHMPSHLGTYY
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zing gene expression in human fetal liver
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Pred. No. 7.9e-65;
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA4135). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed appectification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single
hearts
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                                                                                                                                  DKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP-
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                                             -HGKRYAYKFDFHGIAQALQPH
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure genome the presiston in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                       31.0%;
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                                         HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes
                                                                                                                                                                                                                                                                  ω,
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                                                                                                                                                                                                                                                                                       Score 801; DB 22; Pred. No. 7.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for analyzing gene expression
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                                                                                                                                                                                                                                                                                                            Length 188;
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NTRLPTSHMPSHLGTYY 188

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RESULT 10
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Best Local S
Matches 151
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bor samples, which may enable the improved diagnosis and treatment such as lymphoma, leukaemia and myeloma. The present sequence protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM67391 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid
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NTRLPAAHMPSHLGTYY
                                                                         PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPDALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                                                DKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTRLPTSHMPSHLGTYY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                       LTSLGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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cancer; leukaemia; lym;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27697; 658pp + Sequence Listing;
                                                                                                                       HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                         Score 801; DB 22; Pred. No. 7.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphoma;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
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                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                     40;
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Best Local S
Matches 151
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENP are derived from human HeLa cells. The SENP are derived from human gene be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                      Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                Claim 27;
                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488901/53.
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #1655 encoded by probe
                                                                                                                           Local 151;
                                                                                                                                                                                                                                          cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
112
                                                                  362
                                                                                                              302 LANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY
                                           72
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                                                        DKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP-
                                                                                       PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                                                                                                                                                                                                                                genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human;
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                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                    gene expression
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                      Conservative
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2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                               No 20047;
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                                                                                                                                              31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
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                                                                                                                                                                                                                                                                                                                                            487pp;
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                                                                                                                                                                                                                                                                                                                                                                    exon nucleic acid probes useful for human cervical epithelial cells -
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                                                                                                                                              Score 801; DB 22; Pred. No. 7.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for measuring cervical gene expression.
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                  or form part of the printed format directly from WIPO
                                                                                                                                                         Length 188;
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                           Claim 27;
                                                                                                                                                                                                                                                                                                                               analyzing
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #1719 encoded by probe
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                                                                                                                                                                                                                                   human genetic disorders.
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                                                                                    72
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NTRLPTSHMPSHLGTYY 188
                                                                                               DKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP-
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                                                                                                                            LANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 361
                     NTRLPAAHMPSHLGTYY 478
                                          PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                    DKLSRALRYYDKNIMTKV--
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                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful ring gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTRLPAAHMPSHLGTYY
                                                                                                                                                                       151;
                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
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2000US-0236359.
                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                         27951; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                               31.0%;
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                                                   -HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                     Score 801; DE Pred. No. 7.9e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring placental gene
                                                                                                                                                                               DB 22;
.9e-65;
                                                                                                                                                                                         Length 188;
                                                                                                                                                                     Indels
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RESULT 13
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ID AAM02
XX AAM022
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PR 20-
XX PR 20-
PR 26-
PR 27
PR 21
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Matches 151
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel single exon nucleic acid probes (see Aa100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases include: breast cancer, disorders of proliferative breast diseases and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO and the property of the property can be proportionally the property and the property can be proportionally the property of the printed and property of the printed property of the property of the property of the printed property of the printed property of the p
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at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel single exon nucleic acid in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM02964 standard;
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                                                                          421
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                                                                                                                                                                                                                                                                                                                      302 LANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 361
                                                                                                                                              72
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                                                                                                                                                                                   DKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP- 420
                                                                                                                                                                                                                                                                                 LTSLGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNY 71
PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
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                                                                                                                                              DKLSRALRYYDKNIMTKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                          151;
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2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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76.6%;
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                             --HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 801; DB 22; Pred. No. 7.9e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for measuring breast gene
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                                                                                                                                      HGKRYAYKFDFHGIAQALQPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 14
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      nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                            measure
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG37017 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single exon probe; asthma; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                          gene expression
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2000US-207456P
2000US-060840B
2000US-0632366
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             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener Syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertic and hyaline membrane disease. The present sequence is a peptide/pierosed by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exons should be assigned to a single gene; a peptide comprising of 12011 sequences, mentioned in the specification, or encoded by t probes/open reading frames (ORF). The probes are used for gene
                                                                                                                         30-JAN-2001;
                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                           01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                   ABB31070 standard;
                                                                                                                                                                                  WO200157271-A2
                                                                                                                                                                                                                                                     Human; microarray;
                                                                                                                                                                                                                                                                                  Peptide #3721
                                                                                                                                                                                                                                                                                                                                        ABB31070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarrays having a probe with the exon, where a common expression of the exons in the tissues and/or cell types
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTRLPAAHMPSHLGTYY 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSLGSGQIQLWQFLLELLSDSSNSSCITWEGINGEFKMTDPDEVARRWGERKSKPNMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                       NTRLPTSHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLSRALRYYDKNIMTKV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                           2001WO-US00662
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                  encoded
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                                                                                                                                                                                                                                                     single exon probe;
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                                                                                                                                                                                                                                                                                                                                                                   Peptide;
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                                                                                                                                                                                                                                                   gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
.9e-65;
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(MOLE-) MOLECULAR DYNAMICS INC.

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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less blas than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                             probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 14038; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon
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                                                                                                                                                                                            379
                                                                              101 SYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN 144
                                                                                              421 --HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN 462
                                                                                                                                                                                                                                                                     319 LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT 378
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Pred. No. 6.2e-51;
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(c) 1993 - 2002 Compugen Ltd
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US-08-878-177-4
US-08-343-443B-4
US-09-360-779-2
US-09-360-779-2
US-09-435-335-2
US-09-055-113-4
US-09-055-113-4
US-09-055-113-7
US-08-469-412A-7
US-09-021-715-2
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Sequence 4, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: chugaí seíyaku kabushiki kaisha 5001
CURRENT APPLICATION NUMBER: US/08/878,177
CURRENT FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08878177
Patent No. 6294354
GENERAL INFORMATION:
APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, I
TITLE OF INVENTION: Cell Calcification Suppressing
TITLE OF INVENTION: the Proteins
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Best Local
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86.3%; Pred. No. 9.9e
Live 0; Mismatches
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Matches 291
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Weiser, Gerard J.
REGISTATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text ed
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: UUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR 92/06123 FILING DATE: 20-MAY-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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STATE:
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                   TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR 178
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DQSSRLSVKEDPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGP
                                                                  ATTLYNTEVLLSHLSYLRESSL---
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230 South Fifteenth Street
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Peter, Martine
Ploougastel, Be
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Conservative 55
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18-NOV-1994
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Pred. No. 8.8e-134;
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              Sequence 2, Application US/09435335
Patent No. 6384204
GENERAL INFORMATION:
APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounting OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-04027
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EARLIER APPLICATION NUMBER: 60/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-03828
FILE REFERENCE: CASE-03828
CURRENT APPLICATION NUMBER: US/09/360,779
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                                                                                                                                                                                                                                                                                                           QACQPPPAHAHAAAAAAAAAAAAQDGALYKLPAGLAPLPFPGLSKLNLMAASAGVAPAGF
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 APPLICATION
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NUMBER: US/09/435,335
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US-09-092-636-9
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APPLICANT: Goldman, Daniel
APPLICANT: Sapru, Mohan K.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 115; Conserv
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 9
LENGTH: 468
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Best Local Similarity 45.3%;
Matches 105; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: UMI-003
CURRENT APPLICATION NUMBER: US/09/092,636A
CURRENT FILING DATE: 1998-06-05
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EARLIER APPLICATION NUMBER: 09/
EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neuregulin Response Element
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                                                                                                                                                                                   DFVGDILWEHLEQMIKENQEKTEDQYEENSHLNAVPHWINSNTLGFSMEQAPYGMQAPN-
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Pred. No. 5.3e-37;
l3; Mismatches 36
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Pred. No. 1
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RESULT 8
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                                                                 Sequence 4, Application US/09055113
Patent No. 6265565
GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENCTH: 470
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GENERAL INFORMATION:
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Best Local
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APPLICANT:
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TITLE OF INV
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NT: Bandman, Olga
NT: Corley, Neil C.
NT: Guegler, Karl J.
NT: Lal, Preeti
F INVENTION: PROSTATE
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Pred. No. 2.7e-31;
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  K-EPGQRLLFRF 419
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US-09-055-113-4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: GenBan
CLONE: 511283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEO for Wir
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/0 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 SPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPN-MTTNERRVIVPA----DPTLWS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TPAQCSIKQERISYTPPESPVPSYAS-STPLHVPVPRALRMEEDSIRLPAHLRLQPIYWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
KVHPPESSMYKY 390
                                                                                     LSDSSNSNCITWEGTNGE-FKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT 378
                                                                                                                                  QSRLSEDGLHREGKPINLSHREDLAYMNHIMVSVSPPEEHAMPIGRIADCRLLWDYVYQL
                                                                                                                                                                                                                                                                                                                                                                    ARNTGGATFIFPNTSVYPEATQRITTRP-----DLPYEQAR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDDVAQWLKWAENEFSLRPIDSNTFE-MNGKALLLLTKEDFRYRSP-HSGDVLYELLQHI 120
                                          LSDSRYENFIRWEDKESKIFRIVDPNGLARLWGNHKNRTNMTYEKMSRALRHYYKLNIIR
                                                                                                                                                                                                                            VSPMENNHCPASSESHPKPSSPRQESTRVI-----QLMPSPIMHPLILNPRHSVDFK 288
                                                                                                                                                                                                                                                                         -----RSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGP------T
                                                                                                                                                                                                                                                                                                                      RSRSP----ITTNHRPSPDPEQRPLRSPLDNMIRRLSPAERAQGPRPHQENNHQESYPLS
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Pred. No. 6.4e-22;
1; Mismatches 127;
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RESULT 10
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Sequence 7, Application US/09021715
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                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                       Local
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                DMGLAGGAVPQSAPPVPSGGSHFRFPPSTPSEVLSPTEDPRSPPACSSSSSSSSS 167
                                                                                                                                                                                                                    SSPGSRQIQLWHFILELLRKEEYQGVIAWQGDYGEFVIKDPDEVARLWGVRKCKPQMNYD 71
                                                                                                                  --GIAQALQPHAHP----
                                                                                                                                                     KLSRALRYYNKRILHKT-----
                                                                                                                                                                                   KLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFH------ 412
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                                                                                                                                                                                                                                                                                         Conservative
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(415) 576-0300
)R SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                     11.7%; Score 303.5; DB 2; 39.2%; Pred. No. 1.7e-20;
                                                                                                                                                                                                                                                                                                                                                                      /note= "murine ERF amino acid sequence
(first 8 amino acids from first exon not
included)"
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                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                -QKMNFVAP-----HPPALPVTSSSFFAA 447
                                                                                                                                                   -KGKRFTYKFNFNKLVLVNYPFI 111
                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                       Length 543;
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RESULT 11
US-08-469-412A-2
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                                                      Sequence 2, Application US/08469412A Patent No. 5856125
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Mavrot
APPLICANT: Blair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7
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                                                                                                                                                                                                                                                                      363 KLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFH------ 412
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                                                                                                                                                                                                            413 -- GIAQALQPHAHP-----
                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                             12 SSPGSRQIQLWHFILELLRKEEYQGVIAWQGDYGEFVIKDPDEVARLWGVRKCKPQMNYD 71
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-Feb-198
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mavrothalassitis,
Blair, Donald G.
                                                                                                                                                                        DMGLAGGAVPQSAPPVPSGGSHFRFPPSTPSEVLSPTEDPRSPPACSSSSSSLFSA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                    KLSRALRYYNKRILHKT----
                                                                                                                                                                                                                                                                                                                                                                                                             69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first 8 amino acids from first exon included)"
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  Mavrothalassitis, George J. Blair, Donald G.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 303.5; DB 4
Pred. No. 1.7e-20;
6; Mismatches 40
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                                                                                                                                                                                                            -QKMNFVAP-----HPPALPVTSSSFFAA 447
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                                                                                                                                                                                                                                                  -KGKRFTYKFNFNKLVLVNYPFI 111
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US-09-021-715-2
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                                                                                                                                                                                                                                                                  Sequence 2, Application US/09021715
Patent No. 6194547
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 015280-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 548 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                      NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CONNESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                      Athanasiou, Meropi A.
Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GIAQALQPHAHP-----QKMNFVAP-----HPPALPVTSSSFFAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLSRALRYYYNKRILHKT-------KGKRFTYKFNFNKLVLVNYPFI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFH------ 412
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Similarity 39.2%;
69; Conservative 1
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CITY: San Francisco
STATE: California
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INVENTION: The ERF Genetic Locus and Its
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                                                                                                                                                                                                                                             Mavrothalassitis, George
                                                                                                                                                                                    Beal Jr., Gregory J.
                                                                                                                                                                                                         Fisher, Robert J.
                                                                                                                                                                                                                            Blair, Donald G.
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Pred. No. 1.7e-20;
6; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 -- GIAQALQPHAHP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 KLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFH------- 412
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                         COUNTRY: UZIP: 19102
                                                                                                                            CITY: Philadelphia
                                                                                                                                                                  ADDRESSEE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-reb-198
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330
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                                                                                                                                             E: Weiser & Associates
230 South Fifteenth Street
                                                                                          USA
                                                                                                                                                                                                                                                                                                                Zucman, Jessica
                                                                                                                                                                                                                                                                                                                               Ploougastel, Beatrice
Thomas, Gilles
                                                                                                                                                                                                                                                                                                                                                                 Peter, Martine
                                                                                                                                                                                                                                                                                                                                                                                    Melot, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                     Delattre, Olivier
Desmaze, Chantal
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 PC-DOS/MS-DOS
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Pred. No. 1.7e-20;
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RESULT 14
US-09-055-113-1
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                  OPERATING SYSTEM: DOS
SOFTMARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,113
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                   STREET: 31.
STREET: CA CITY: CA CATE: CA
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lal, Preeti
                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Weiser, Gerard
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 19-MAY-1993
                                                                          FILING DATE:
                                                                                      APPLICATION NUMBER:
                                                                                                                                                                          OPERATING SYSTEM:
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57; Conserv
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RESULT 15
US-08-469-412A-11
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US-09-055-113-1
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                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08469412A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mavrothalassitis, Gec
APPLICANT: Blair, Donald G.
APPLICANT: Fisher, Robert J.
APPLICANT: Beal Jr., Gregory J.
APPLICANT: Athanasiou, Meropi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 APPLICANT: Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 335 amino acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMEDIAL FROM LIBRARY: PROC. 1813005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 KALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQS
                                                                                                                                STREET: 'I'WO .....
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 MYKY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 KATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQ-IQLWQFLLE-LLSDSSNSN 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 YRLPPMG-KAFQELAGKELCAMSEEQFRQRSP-LGGDVLHAHL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 YGLPDVDILLFQNIDGKELCKWTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 P---GGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPMDWSPSNVQKWLLWTEHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GMNYGSYMEEKHI--PPPNMTTNE------RRVIVPADPTLWSTDHVRQWLEWAVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                COUNTRY:
                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 YPEDSSWAAKAPGASSREEPP-------EEPEQCPVIDSQAPAGSLDLV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 YGQTSKMSPRVPQQDWLSQPPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGIIRKPDISQRL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                  94111-3834
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                                                                                                                                                               Two Embarcadero Center, Eighth Floor
                                                                                                                  USA
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650-845-4166
                                                                                                                                                                                                                                                                                                                               Mavrothalassitis, George J.
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                 Patentin Release #1.0,
                                                                                                                                                                                Townsend and Townsend and Crew LLP
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26.4%;
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Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4e-19
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APPLICATION NUMBER: US/08/469,412A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: GAITETT-Wackowski, Eugenia

REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 015280-229000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRATURE:

NAME/KEY: Domain

LOCATION: 1.78

OTHER INFORMATION: ets-like ERF DNA-bi;

US-08-469-412A-11

10.98; Score 283;
                                                                             밁
                                                                                                                Ş
                                                                                                                                                     Query Match 10.9%; Score 283; DB 2; Length 78; Best Local Similarity 55.1%; Pred. No. 7e-20; Matches 54; Conservative 10; Mismatches 14; Indels
                                                                       372 YDKNIMTKYHPDESSMYKYPSDLPYMSSYHGKRYAYKF 409
61 YDKNIIHKT------AGKRYVYRF 78
                                                                                                                                                                                                                                                  /note= "ETS1 homologous region to
ets-like ERF DNA-binding domain"
                                                                                                                                                       20;
                                                                                                                                                       Gaps
                                                                                                                                                       1;
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멍 Ş Search completed: November 9, 2002, 16:55:38 Job time: 24.6249 secs

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Database
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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2588
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92612 seqs, 14418503 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November
                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA: *
: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9, 2002, 16:53:32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Search time 37.5608 Seconds (without alignments) 183.490 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	89	7	6	Çī	4	ω	N		Result No.
201.5	209.5	227.5	244	244.5	263.5	263.5	270.5	279	280.5	290.5	290.5	302	302	317	348	472	647	801	Score
7.8	8.1	8.8	9.4	9.4	10.2	10.2	10.5	10.8	10.8	11.2	11.2	11.7	11.7	12.2	13.4	18.2	25.0	31.0	Query Match Length
114	406	325	304	303	551	551	335	55	203	335	335	623	623	452	344	340	144	188	ength I
10	10	10	10	10	12	10	10	10	10	10	10	9	9	10	10	10	10	10	BU
US-09-126-945B-3	US-09-925-301-1049	US-09-841-963A-4	US-09-764-864-1107	US-09-925-297-768	US-10-033-528-1789	US-09-920-300A-1789	US-09-841-963A-2	US-09-864-761-40154	US-09-925-297-716	US-09-866-356-1	US-09-126-945B-2	US-10-108-605-129	US-10-108-605-125	US-09-866-356-4	US-09-925-300-1360	US-09-850-799-2	US-09-864-761-36929	US-09-864-761-34947	ID
Sequence 3, Appli	Sequence 1049, Ap	Sequence 4, Appli	1107,	Sequence 768, App	Sequence 1789, Ap	Sequence 1789, Ap		Sequence 40154, A	716	Sequence 1, Appli	Sequence 2, Appli	Sequence 129, App	Sequence 125, App	Sequence 4, Appli	Sequence 1360, Ap	Sequence 2, Appli	Sequence 36929, A	Sequence 34947, A	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	2
96.5	97	97	97.5	97.5	97.5	98	98	101.5	103.5	106.5	106.5	106.5	109	109.5	111.5	111.5	112	114.5	116	125.5	169	193	193	193.5	201.5
3.7	3.7		3. 8						4.0	4.1	4.1	4.1	4.2	4.2	4.3	<u>4</u> د.	4.3	4.4	5	4.8	6.5	7.5	7.5	7.5	· a
2441	888	521	630	507	507	743	743	4019	476	2063	2005	1070	1464	760	939	939	1736	796	64	51	71	36	36	371	<b>114</b>
12	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	5
US-10-109-886-8	US-09-826-752-6	US-09-749-728B-19	US-09-801-368-220	US-09-749-728B-13	US-09-876-187-2	771	US-09-771-161A-164	US-09-738-973-425	US-09-815-242-11910	US-09-735-367B-2	US-09-735-367B-3	US-09-735-367B-6	US-09-842-256-2	US-09-746-801A-27	US-09-801-368-380	US-09-226-248B-29	US-09-919-497-98	US-09-801-368-30	US-09-864-761-47397	US-09-864-761-44339	US-09-864-761-43109	US-09-864-761-45584	US-09-864-761-38205	US-09-922-217-1109	US-U9-800-350-3
Sequence 8, Ap	Sequence 6, Ap	Sequence 19, 1	∵	Sequence 13, 1	Sequence 2, Ap	Sequence 254,	Sequence 164,	Sequence 425,	Sequence 1191(			Sequence 6, Ap	Sequence 2, Appli		Sequence 380,	Sequence 29, 1	Sequence 98, 1	Sequence 30, 1		Sequence 44339	Sequence 43109	Sequence 45584	Sequence 38205	Sequence 1109,	sequence 3, Ap
Appli	Appli	Appl	App	Appl	ppli	4, App	Āpp	App	0, A	ppli	ppli	ppli	ppli	Appl	App	App1	App1	, Appl	7, A	9, A	9, A	4 , A	5, A	, Ap	Appli

### ALIGNMENTS

US-09-864-761-34947 ; Sequence 34947, Application US/09864761 ; Patent No. US20020048763A1 ; GENERAL INFORMATION:

APPLICANT: Penn, Sharron APPLICANT: Rank, David H

Rank, David R.

PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR PRIOR PRIOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY APPLICANT: PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR FILING DATE: 2001-01-30 FILE REFERENCE: Aeomica-X-1 PRIOR APPLICATION NUMBER: PCT/US01/00664 APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30 Hanzel, David K. Chen, Wensheng

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US-09-864-761-36929
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; OTHER INFORMATION:
US-09-864-761-34947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36929, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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LENGTH: 188
                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn,
APPLICANT: Rank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HOMO S
FEATURE:
OTHER INFORMATIC
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18
TYPE: PRT
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HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4

PHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 1.4

PHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.92

PHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

PHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

PHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

PHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

PHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5

PHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

PHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

PHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

PHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

PHER INFORMATION: SWISSPROT HIT: BE831331.1, EVALUE 4.00e-65

PHER INFORMATION: SWISSPROT HIT: P11308, EVALUE 8.00e-99
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Hanzel, David K.
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Pred. No. 2.8e-58;
3; Mismatches 3
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CREATURE: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO APO00021.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FALL, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HELION, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 
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Best Local S
Matches 123
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101
                                                           421 -- HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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Pred. No. 6.8e-46;
1; Mismatches 0;
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RESULT 3
US-09-850-799-2
; Sequence 2, Application US/09850799
; Patent No. US20020090647A1
; GENERAL INFORMATION:

APPLICANT: Deneris, Evan APPLICANT: Fyodoro, Dmit APPLICANT: Hendricks, Ti

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                                                                                                                                                                                                                 ; OTHER INFORMATION: US-09-925-300-1360
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Steve Ruben
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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                                                                                                                                      Matches
                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Craig Rosen APPLICANT: Steve Ruber
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SOFTWARE: PatentIn Ver
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CURRENT FILING DATE: 2001-05-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/360,779

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases FILE REFERENCE: CASE-03828
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
LOCATION: (2)
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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206 DDVDKALQNSPRLMHARN--TGGAT---
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                                                                                           163 IDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRE---
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                                                      MNGQMLCNLGKERFLELAPDFVGDILWEHLEQMIKENQEKTEDQYEENSHLTSVPHWINS 68
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                                                                                                                               13.4%; Score 348; DB 10; 29.2%; Pred. No. 5.6e-21; tive 37; Mismatches 94;
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Pred. No. 4.3e-31;
13: Mismatches 36;
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                FIFPNTSVYPEATQRIT 245
                                                                                                                                                                      Length 344;
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                                                                                           ----TPLPH-LTS 205
                                                                                                                                 102;
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US-09-866-356-4
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                                                                         US-09-866-356-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US Patent No. US20020098543A1 GENERAL INFORMATION:
       Matches
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/055,113
FILING DATE: 1998-04-03
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                          TOPOLOGY: 1i
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROSTATE-ASSOCIATED ETS PROTEIN NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, Olga
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                                                                                                        LIBRARY: GenBank
CLONE: 511283
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/866,356 FILING DATE: 29-May-2001 APPLICATION DATA:
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
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                                                                                                                                                                                                                                                                 TELEX: <Unknown>
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       Conservative
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Lal, Preeti
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                  12.2%;
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     61;
   Score 317; DB
Pred. No. 2.8e
61; Mismatches
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   DB 10;
2.8e-18;
hes 127;
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                                  Length 452;
   Indels 138;
Gaps
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81 SPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPN-MTTNERRVIVPA----DPTLWS 135

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CURRENT APPLICATION NUMBER: US/10/108,605
CCURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SUPPLY OF SER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SUPPLY OF SER OF SEQ ID NO 125
LENGTH: 623
TYPE: PRT
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Best Local S
Matches 68
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Patent No. US20020160934A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bachmann, Ja
APPLICANT: Kamdar, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                         319
    584
                                                                                                                                                                     479 AHQHPAAYMSTL-----
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                                                                                                                                                                                                                                                 Match 11.7%; Score 302; DB 9; Local Similarity 45.0%; Pred. No. 7.4e-17; les 68; Conservative 14; Mismatches 31
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    ZT-
                                       KVHPPESSMYKYPSDLPYMSSYHGKRYAYKF 409
                                                                                LLLDKTCQSFISWTGDGWEFKLTDPDEVARRWGIRKNKPKMNYEKLSRGLRYYYDKNIIH
                                                                                                                       LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRLSEDGLHREGKPINLSHREDLAYMNHIMVSVSPPEEHAMPIGRIADCRLLWDYVYQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDDVAQWLKWAENEFSLRPIDSNTFE-MNGKALLLLTKEDERYRSP-HSGDVLYELLQHI 120
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-AGKRYVYRF 594
                                                                                                                                                                ----GLDK-GLLGGYTTQGGVPCFTGSGPIQLWQFLLE 523
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CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 129
LENGTH: 623
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-108-605-129
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                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-126-945B-2
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US-09-126-945B-2
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US-10-108-605-129
                                                                                                                                                                                                                    FILE REFERENCE: 1488 1090000

CURRENT APPLICATION NUMBER: US/09/126,945B
CURRENT FILING DATE: 1998-07-31

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 335
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                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 68; Conserv
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                                                                      Matches
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APPLICANT: Oettgen, Joerg P.
APPLICANT: Kunsch, Charles A.
APPLICANT: Endress, Gregory A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
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                  41 YGQTSKMSPRVPQQDWLSQPPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KT-----AGKRYVYRF 594
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 302; DB 9; Length 623; ilarity 45.0%; Pred. No. 7.4e-17; Conservative 14; Mismatches 31; Indels
                                                                 11.2%; score 290.5; DB 10; 26.4%; Pred. No. 2.6e-16; tive 41; Mismatches 114;
<del>--</del>
                                                                   Indels 113;
                                                                                                             Length
                                                                                                             335;
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US-09-866-356-1
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                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION UNIMBER: 09/055,113

FILING DATE: 1998-04-03

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0501

TELEPONGUICATION INFORMATION:

TELEPONGUICATION 1050-855-0555
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal, Preeti
TITLE OF INVENTION: PROSTATE-ASSOCIATED ETS PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/866,356
FILING DATE: 29-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                              SEQUENCE CHARACTERISTICS:
                IMMEDIATE SOURCE:
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                                STRANDEDNESS:
TOPOLOGY: line
                                                                          TYPE: amino acid
                                                                                                                                                                      TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
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LIBRARY:
                                                                                            LENGTH: 335 amino acids
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Corley, Neil C.
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-925-297-716
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US-09-925-297-716
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                                          Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acids, Proteins and
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                          LENGTH: 203
120
                                                                                                                                           257 RSAWTSHSHPTQSKATQP-----SSSTVPKTEDQRPQLDPYQIL-GPTSSRLANPGSGQI 310
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                           371 YYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKF 409
                                                                                          311 QLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRY 370
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                                                                                                                                                                                                         Local
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                                                                                                                         RGGYFSSSHEGFSYEKDPRLYFDDTCVVPERLEGKVKQEPTMYREGPPYQR-----RGSL 59
                                                           QLWQFLVTLLDDPANAHFIAWTGRGMEFKLIEPEEVARRWGIQKNRPAMNYDKLSRSLRY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQ-IQLWQFLLE-LLSDSSNSN
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                                                                                                                                                                                                         Score 280.5; DB 1
Pred. No. 8.4e-16;
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Pred. No. 2.
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                                                                                                                                                                                         Indels
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; OTHER INFORMATION: US-09-864-761-40154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 40154
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED
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                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                                                                                                                  INFORMATION:
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                                                                                N: WAP TO AP001426.1

N: EXPRESSED IN PLACENTA, SIGNAL = 2.1

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76

N: EXPRESSED IN HEART, SIGNAL = 2.1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

N: EXPRESSED IN BRAIN, SIGNAL = 2.1
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No. 1
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                   Length 55;
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RESULT 13
US-09-920-300A-1789
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Best Local Similarity
Watches 93; Conserve
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US-09-841-963A-2
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Sequence 1789, Application US/09
Patent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, Dennis K.
APPLICANT: Papas, Takis S. (Deceased)
APPLICANT: Papas, Tula C. (Legal Representative)
TITLE OF INVENTION: Methods and compositions for the diagnosis and
TITLE OF INVENTION: based on transcription factor ETS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US99/27805 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/841,963A CURRENT FILING DATE: 2001-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: based on transcription FILE REFERENCE: 10545-015-999
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                                                                                                                                                                                 VYQF
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Pred. No. 1.1e-14;
3; Mismatches 115;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1789
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-528-1789
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SEQ ID NO 1789
LENCTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-300A-1789
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US-10-033-528-1789
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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
                                                                                                                                 Sequence 768, Application US/09925297 Patent No. US20020081659A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
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                                                                                                                                                                                                                                               296 GPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKS 355
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Xu, Jiangchun
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                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 263.5; DB 12; 46.5%; Pred. No. 8.6e-14;
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (257)
; OTHER INFORMATION: X
US-09-925-297-768
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; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SEQ ID NO 768
; ELENGTH: 303
; TYPE: PRT
Search completed: November Job time: 38.5608 secs
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Result

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Database

transcription fact	S24061	-	555	10.3	266	5
88K E-26-specific	A46193	N	761	10.8	278.5	44
ets-related protei	A46396	N	342	10.8	278.5	Ψ
transcription fact	S43692	۲	510	10.8	280.5	2
lin-1 protein - Ca	T33103	N	393	10.8	280.5	11
transcription fact	B46396	1	477	11.1	288	Ö
transcription fact	I38893	۳	477	11.3	293	39
transcription fact	A45938	N	110	11.6	300.5	38
gene pointed prote	S33167	Ľ	623	11.7	302	37
	S59133	N	548	11.7	303.5	36
PE-1 protein - hum	A54308	N	250	12.2	314.5	35
ETS domain protein	A43315	N	732	12.2	315.5	34
transforming prote	S24300	N	211	12.3	318	3
transcription fact	S11224	N	268	12.6	326	32
transcription fact	S28820	N	94	13.3	344.5	3
gene pointed prote	S33168	H	718	13.5	350.5	30

## ALIGNMENTS

A;Gene: erg
C;Superfamily: transcription factor erg; ets DNA-binding do
C;Superfamily: transcription factor erg; ets DNA-binding do
C;Keywords: DNA binding; phosphoprotein; proto-oncogene; tt
E;119-193/Domain: ets RII regulatory region homology <ETR>
E;312-390/Domain: ets DNA-binding domain homology <ETS> A;Title: Mesodermal expression of the chicken erg gene A;Reference number: S60754; MUID:95329425; PMID:7605748 A;Accession: S60754 transcription factor erg - chicken C; Species: Gallus gallus (chicken) C; Date: 27-Apr-1996 #sequence\_revision C; Accession: S60754 A;Cross-references: EMBL:X77159; NID:g790439; PIDN:CAA54404.1; PID:g790440 C;Genetics: A; Molecule type: mRNA A; Residues: 1-478 < DHO> R; Dhordain, P.; Dewitte, F.; Desbiens, X.; Stehelin, D.; Duterque-Coquillaud, Mech. Dev. 50, 17-28, 1995A; Status: preliminary RLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN TQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQIIGPTSS PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEA PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKNVSSSDNVGMNYGSYMEEKHIPPPNMTT 120 YDKLSRALRYYYDKNIMTKV NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP TQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSS NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT MASTIKEALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQP PSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATF IF PNTSVYPEA Similarity Conservative 94.18; 92.08; 0 Score 2436; Pred. No. 3 Mismatches 23-May-1997 #text\_change 16-Jul-1999 6; DB 1; . 3.3e-164; 0; HPPESSMYKYPSDLPYMSSY Length 478; Indels associated with precartilagino domain homology; ets RII reg transcription factor; transf 40; Gaps 300 180 180 400 300 240 60 60 2 ×

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A:Title: erg, a human ets-related gene on chromosome 21: alternative splicing, polyadeny A; Reference number: A94294; MUID:87263429; PMID:3299708

A:Reference number: A94294; MUID:87263429; PMID:3299708

A; Rosidues: 1-231,256-486 <READ
A; Rosidues: 1-231,256-486 <READ
A; Cross-references: GB-M17254; NID:g182186; PIDN:AAA52398.1; PID:g182187
A; Cross-references: GB-M2734; NID:g182186; PIDN:AAA52398.1; PID:g182187
A; Reddy, E.S.P.; Rao, V.N.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 6131-6135, 1987
A; Title: The erg gene: a human gene related to the ets oncogene.
A; Reference number: A94178; MUID:87317608; PMID:3476934
A; A; Cross-references: GB-M2133; MID:g182182; PIDN:AAA35811.1; PID:g182185
A; A; Cross-references: GB-M2133; MID:g182182; PIDN:AAA35811.1; PID:g182185
A; Cross-referentially spliced erg 3 product functions as a transcriptional activator.
A; Reference number: 158410; MUID:94119611; PMID:8290279
A; A; Cross-referentially spliced erg 3 product functions as a transcriptional activator.
A; Reference number: 158410; MUID:94119611; PMID:8290279
A; Cross-references: GB-M2130; NID:9441960; PIDN:AAA35911.1; PID:g182185
A; Cross-references: GB-S68130; NID:g544960; PIDN:AAA359724.1; PID:g544961
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                                                             SYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEAT
                                                                                                                                            ERRYIYPADPTLWSTDHYRQWLEWAYKEYGLPDYDILLFQNIDGKELCKMTKDDFQRLTP
                                                                                                                                                                                                                                                               ARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTN
                                                                                                                                                                                                                                                                                                                                           HGKRYAYKFDFHGIAQALQPHAHPQKWNFYAPHPPALPVTSSSFFAAPNPYWNSPTGGIY
        SYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGAAFIFPNTSVYPEAT
                                                                                                                                                                                                                                    ARVTIKMECNPSQVNGSRNSPDECSVAKGGKMVGSPDTVGMNYGSYMEEKHMPPPNMTTN
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Pred. No. 2.5e
9; Mismatches
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A; Cross references: EMBL:x67001; NID:g32529; PIDN:CAA47399.1; PID:g32530
A; Title: Human FLI-1 localizes to chromosome 11024 and has an aberrant transcript.
A; Reference number: $29843; MUID:93176799; PMID:8439553
A; A; Cross references: EMBL:M93255; NID:g182659
A; Cross references: EMBL:M93255; NID:g182659
A; Note: the authors translated the codon GTG for residue 69 as Glu
R; Hromas, R.A.; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Beck, E.; I
Submitted to the EMBL Data Library, May 1993
A; Reference number: $35506
A; A; Cross references: EMBL:M93255; NID:g182659; PIDN:AAA58479.1; PID:g182660
A; Residues: 1-68, V', 70-76, 78-129, 'A', 131-132, 'V', 134-322, 'Q', 324-425, 427-452 <HRO:
A; Cross references: EMBL:M93355; NID:g182659; PIDN:AAA58479.1; PID:g182660
R; Prasad, D.D.; Rao, V.N.; Reddy, E.S.
A; Cross references: EMBL:M93353, 1992
A; Title: Structure and expression of human F11-1 gene.
A; Reference number: A49000; MUID:93007976; PMID:1394211
A; Accession: A49000
A; Status: oreliminary
                                                                               A; Molecule type: mRNA
A; Residues: 1-322, 'Q', 324-452 <PRA>
A; Residues: 1-322, 'Q', 324-452 <PRA>
A; Cross-references: GB:S45205; NID:g257353; PIDN:AAB23637.1; PID:g257354
A; Note: sequence extracted from NCBI backbone (NCBIN:115336, NCBIP:115337)
R; Watson, D.K.; Smyth, F.E.; Thompson, D.M.; Cheng, J.Q.; Testa, J.R.; Paper Cell Growth Differ. 3, 705-713, 1992
A; Title: The ERGB/Fli-1 gene: isolation and characterization of a new membra; Reference number: A49015; MUID:93075640; PMID:1445800
A; Accession: A49015
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-390,'Q'
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N;Alternate names: Friend
C;Species: Homo sapiens (m
C;Date: 04-Oct-1996 *seque
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A; Residues: 1-452 <DE
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Species: Homo sapiens (man)
Date: 04-Oct-1996 #sequence_revision 30-May-1997 #text_change 03-Mar-2000
Accession: I37565; S29843; S35506; A49000; A49015; I54170
Delattre, O.; Zucman, J.; Plougastel, B.; Desmaze, C.; Melot, T.; Peter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
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YDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP
                                                                                                                                                                                                                                                                                                           QRITTRPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQIIGPTSS
HPPESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYMNSPTGGIY
                                                                                                                                                                                       RLANPGSGQIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN
                                                                                                                                                                                                             RLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMN
                                                                                                                                                                                                                                                                                  QRITTRPDLPYEPPRRSAWTGHGHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSS
                                                                                             HGKRYAYKFDFHGIAQALQP
                                              460
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human protein 1; transcription factor

R;Delattre, O.; Zucman, J.; Plougastel, B.; Desmaze, C.; Melot Nature 359, 162-165, 1992
A;Title: Gene fusion with an ETS DNA-binding domain caused by A;Reference number: S28257; MUID:92396239; PMID:1522903
A;Accession: 137565 chromosome translocatio . .

from GB/EMBL/DDBJ

aberrant transcript [1] Klems

expressed [F] ...

Papas,

new member

of. T.S.;

the

S

RII

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RESULT 4
S17403

transforming protein fli - mouse
N;Alternate names: Friend leukemia integration protein 1;
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_c;
C;Accession: S17403
R;Ben-David, Y; Giddens, E.B.; Letwin, K.; Bernstein, A.
Genes Dev. 5, 908-918, 1991
A;Title: Erythroleukemia induction by Friend murine leukem
A;Reference number: S17403; MUID:91257578; PMID:2044959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:FLI1
A;Cross-references: GDB:127565; OMIM:193067
A;Cross-references: GDB:127565; OMIM:193067
A;Map position: 11q24.1-11q24.3
A;Map position: 77/3
A;Introns: 77/3
A;Introns: 77/3
A;Introns: 77/3
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII reguce; Superfamily: transcription factor erg; bnA binding; nucleus; proto-oncogene; transcription C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription F;118-192/Domain: ets RII regulatory region homology <ETR>
F;283-361/Domain: ets DNA-binding domain homology <ETS>
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A;Note: sequence extracted from NCBI backbone (NCBIN:119390, NCBIP:119392)
R;Baud, V; Lipinski, M; Rassart, E; Poliquin, L; Bergeron, D.
Genomics 11, 223-224, 1991
A;Title: The human homolog of the mouse common viral integration region, FLI1,
A;Reference number: I54170; MUID:92112219; PMID:1765382
A;Accession: I54170
A;Accession: I54170
A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBI
A;Molecule type: DNA
A;Residues: 1-6 <BAU>
A;Cross-references: GB:L47616; NID:g1000863; PIDN:AAA76854.1; PID:g1000864
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                                                                                                                                                                                                                                                          GIYPNPNVPRHPNTHVPSHLGSYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \verb"MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ"
                                                                                                                                                                                                                                                                                                                                                                        LQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
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nilarity 57.7%;
Conservative 5
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Pred. No. 6
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6e-97;
                                                                                                                                      protein 1;
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C; Geneti A; Gene: C; Superf C; Keywor F; 117-19

;Genetics:

;Superfamily: transcription factor erg; ets DNA-binding domain ;Keywords: DNA binding; nucleus; proto-oncogene; transcription ;117-191/Domain: ets RII regulatory region homology <ETR>

PIDN:CAA47389.1;

PID:9505487

homology; ets RII factor; transformi

transforming

transforming protein fli - African clawed frog N; Alternate names: Friend leukemia integration C; Species; Xenopus laevis (African clawed frog) C; Date: 07-May-195 #sequence\_revision 23-May-1 C; Accession: \$49013

23-May-1997

#text\_change 16-Jul-1999

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C;Accession: \$49013
R;Mech. Dev. 44, 109-121, 1993
A;Title: X1-fli, the Xenopus homologue of the fli-1 gene, A;Reference number: \$49013; MUID:94206844; PMID:8155576
A;Accession: \$49013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-453 <MEY>
A;Cross references: EMBL:X66979; NID:g505486; PIDN:CAA4738

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A;Accession: S17403
A;Molecule type: mRNA
A;Residues: 1-452 <BEN>
A;Cross references: GB:X59421; NID:g50974; PIDN:CAA42055.1; PID:g50975
C;Genetics:
A;Gene: Fli
C;Superfamily: transcription factor erg; ets DNA-binding domain homolog
C;Kuywords: DNA binding; nucleus; proto-oncogene; transcription factor
E;118-192/Domain: ets RII regulatory region homology <ETR>
F;283-361/Domain: ets DNA-binding domain homology <ETS>
RESULT
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Matches 291
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                                                       GIYPNPSVPRHPNTHVPSHLGSYY
                                                                                                                                                                                        NMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQA 417
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                                                                                                              LQPHPTETSMYKYPSDISYMPSYHAHQQKVNFVPSHPSSMPVTSSSFFGAASQYWTSPTA
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57.7%;
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                                                                                                                                           HAHPOKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTG
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Pred. No. 2.2e-96;
3; Mismatches 82;
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                                                       452
                                                                                                                                                                       -HGKRYAYKFDFHGIAQA
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MOI. Cell. Biol. 13, 7163-7169, 1993
A.Title: Ets proteins: new factors that regulate immunoglobulin heavy-chain gene A.Title: Ets proteins: new factors that regulate immunoglobulin heavy-chain gene A.Title: Ets proteins: new factors that regulate immunoglobulin heavy-chain gene A.Title: Ets proteins: new factors that regulate immunoglobulin heavy-chain gene immunoglobulin heavy-chain gene immunoglobulin heavy-chain gene immunoglobulin heavy-chain gene immunoglobulin heavy-chain selection: A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-272 <RIV>
A.Molecule type: mRNA
A.Residues: 1-272 <RIV>
A.Cross-references: GB.566169; NID:g436276; PIDN:AAB28525.1; PID:g436277
A.Experimental source: pre-B-cell line 22D6
A.Note: sequence extracted from NCBI backbone (NCBIN:138523, NCBIP:138524)
C.Superfamily: transcription factor erg; ets DNA-binding domain homology: ets RII
C.Keywords: DNA binding; phosphoprotein; proto-oncogene; transcription factor; tr
                                                                                                                                                                                                                                                                                                                             transcription factor erg - mouse (fragment)
N;Alternate names: Ig heavy chain enhancer-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A54617
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57.4%;
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                                                                         Score 1253.5;
Pred. No. 3.8e
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Pred. No. 5.16
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3.8e-81;
8;
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5.1e-94;
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Best Local :
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Residues: 1-385 <HRO>
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56.8%;
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¥	234	234 TSVYPEATQRITTRPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPY 292	
ŏ	61	61 TSVYPEATQRITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQPSPSAVPKTEDQRPQLDPY 120	
¥	293	293 QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE 352	
ŏ	121	121 QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE 180	
Ÿ	353	RKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSY	
ŏ	181	RKSKPNMNYDKLSRALRYYYDKNIMTKV	
Ÿ	413	413 GIAQALQPHAHPQKMNFVAPHPPALPVTSSSF 444	
ŏ	221	HPPESSLYKYPSDLPYMGSY	

RESULT 7
\$29844

transforming protein fli, short splice form - human

N;Alternate names: Friend leukemia integration protein 1; transcription
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence\_revision 23-May-1997 #text\_change 16-Jul-:
C;Accession: \$29844
R;Hromas, R.; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Be Biochim. Biophys. Acta 1172, 155-158, 1993
A;Title: Human FLI-1 localizes to chromosome 11024 and has an aberrant 1
A;Reference number: \$29843; MUID:93176799; PMID:8439553
A;Accession: \$29844
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Bolecule type: mRNA
A;Bolecule type: mRNA
A;Bolecule type: mRNA
A;Bolecule type: mRNA A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1992 C;Genetics:
A;Gene EDB:FLI1
A;Cross-references: GDB:127565; OMIM:193067
A;Cross-references: GDB:127565; OMIM:193067
A;Map position: 11q24.1-11q24.3
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII reg C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription F;52-126/Domain: ets RII regulatory region homology <ETR>F;217-295/Domain: ets DNA-binding domain homology <ETS> A;Residues: 1-385 <HKU->
A;Cross-references: EMBL:M93255; NID:g18265; FA;Note: the nucleotide sequence was submitted Date: 02-Dec-1993 #sequence\_revision 23-May-1997 #text\_change 16-Jul-1999 PIDN: AAA58480.1; PID: g182661 protein 1; transcription DB 1; Length aberrant transcript R.A.; not Beck, shown factor [2] Klems

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SRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNMTTNERRVIVPADPTLWST 136 44; Mismatches Score 1232.5; Pred. No. 1.96 No. 1.9e-79; 65; Indels 75; Gaps 7;

DHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLR 196 EHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLR ARESPYDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNMTTNERRVIVPADATLVTQ 129 69

ETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQAR -----LAYNTTSHTDQSSRLSVKEDPSYDSVR 160 256

RGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANPGSGQIQLWQF RSAWTSHSHPTQSKATQ-PSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQF 315

280 375

IMTKV-----IMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP----HGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDIS 320 420

HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN---TRLPAAHMPS :: = = : 472

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transcription factor erg/fl1-1 homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 16-Jul-1999
C;Accession: A56646
R;Oi, S:; Chen, Z.Q.; Papas, T.S.; Lautenberger, J.A.
DNA Seq. 3, 127-130, 1992
A;Title: The sea urchin erg homolog defines a highly conserved erg-specific A;Reference number: A56646; MUID:93091246; PMID:1457815
A;Accession: A56646
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A;Residues: 1-173 <QIA>
A;Cross-references: GB:M81067; NID:g161310; PIDN:AAA68905.1; PID:g161311
A;Cross-references: GB:M81067; NID:g161310; PIDN:AAA68905.1; PID:g161311
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets:C;Keywords: DNA binding; nucleus; transcription factor F;6-84/Domain: ets DNA-binding domain homology <ETS>
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$51226
$51226

transcription factor erg/fli-1 homolog - polychaete (Nereis diversicolor) (fragment)
C;Species: Nereis diversicolor (sandworm)
C;Date: 15-Jul-1995 #sequence_revision 23-May-1997 #text_change 30-May-1997
C;Accession: $51226
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                                                                                                                                                             C;Superfamily: transcription factor erg; ets DNA-binding C;Keywords: DNA binding; nucleus; transcription factor F;7-85/Domain: ets DNA-binding domain homology <ETS>
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A; Accession: S51226
A; Status: preliminary
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FEBS Lett. 354, 62-66
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A; Residues: 1-179 <LEL>
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                        GSGQIQLWQFLLELLSDSANSHIITWEGTNGEFKLVDPDETARRWGERKSKPNMNYDKLS
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                                                                                                                                                                                                                                                                                                                                            A.; Laudet, V.; Flourens, A.; Begue, A.; Leprince, D.; Fontaine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
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                                                                                                           21.7%;
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                                                                                           Score 560.5;
Pred. No. 1.66
L4; Mismatches
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Pred. No. 4.8e-35;
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                                                                                           .5; DB 2;
1.6e-32;
ches 25;
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transcription factor elg - fruit fly (Drosophila melanogaster) (R)Alternate names: transcription factor ets-97D C;Species: Drosophila melanogaster C;Date: 13-Jan-1995 #sequence_revision 23-May-1997 #text_chang C;Accession: S37616; S28822 R;The, S.M.; Xie, X.; Smyth, F.; Papas, T.S.; Watson, D.K.; Sc
                                                                                                           RESULT 11
S37616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T08H4.3 - Caenorha C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision C;Accession: T34343
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A; Residues: 1-377 <STE>
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Best Local S
Matches 133
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133; Conserv
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A;Map position: 2
A;Introns: 63/3; 88/1; 111/3; 146/1; 194/1; 297/1; 343/3
C;Superfamily: ets DNA-binding domain homology
F;216-294/Domain: ets DNA-binding domain homology <ETS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U39470; PIDN:AAC71120.1; GSPDB:GN00020; A;Experimental source: strain Bristol N2; clone T08H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1995
A; Description: The sequence of C. elegans cosmid T08H4.
A; Reference number: Z21510
A; Accession: T34343
                                                                                                                                                                                                                                                                                                                                                                                                                                     210 KALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 DVDILLFQNID--GKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDV--D
                           SYHGKRYAYKFDFHGIAQALQP--HAHPQ-----KMNFVAP
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                                                                                                                        KMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMS
                                                                                                                                                                                            KLSNSTSFANPDPYQILGPTSKNLAHSGSGQTQLWQFLLELLSDKRYSEVITWEGTQGEF
                                                                                                                                                                                                                                                                                        GAAATSGSNGSSSSTESKSDVFNISMNAFAATPGS----KSEDHNIPSFNMLSSYYTGAL
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                                                                                                                                                                                                                                                                                                                                          -----PTQSK-----ATQPSSSTVPKTEDQR-PQL-----
                                                                                                                                                                                                                                      DPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 506.5; DB 38.9%; Pred. No. 3e-28; tive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FPFFNGMQNDFPPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 377;
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                                                                                               284
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#text\_change 16-Jul-1999

Schulz, R.A.

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hypothetical protein C42D8.4 - Caenorhabditis ele
C; Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-199
C;Accession: T15790
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid
A;Reference number: Z18405
A;Reference number: Z18405
A;Accession: T15790
A;Status: preliminary; translated from GB/EMBL/DI
A;Molecule type: DNA
A;Residues: 1-208 <HALD
A;Residues: 1-208 <HAL>
A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293845;
A;Experimental source: strain Bristol N2; clone C42D8
C;Genetics:
A;Gene: CESP:C42D8.4
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C;Superfamily: transcription factor elg; ets DNA-bind C;Superfamily: transcription factor C;Keywords: DNA binding; nucleus; transcription factor F;190-263/Domain: ets RII regulatory region homology F;348-426/Domain: ets DNA-binding domain homology <FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the authors translated the codon AGC: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Isolation and characterization of A; Reference number: S28819; MUID:92249640; A; Accession: S28822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 7, 2471-2478, 1992
A;Title: Molecular characterization and structural organization of D-elg, A;Reference number: 837616; MUID:93096481; PMID:1461651
A;Accession: S37616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <THE>
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A;Cross-references: FlyBase:FBgn0004510
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A; Residues: 298-449 <CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 NQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPP-----PNMTTNERRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                               SSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPN
: : ||:||||||:|:||
---IGSGNNGQVQLWQFLLEILTDCEHTDVIEWVGTEGEFKLTDPDRVARLWGEKKNKPA
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                                                                                                                                                                                                                                                                                                                                                 MNYEKLSRALRYYDGDMISKV
                                                                                                                                                                                                                                                                                                                                                                                 MNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.70
0; Mismatches
                                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                                                            20-Sep-1999 #text_change 02-Sep-2000
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cosmid C42D8
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                                                      PIDN: AAA98717.1;
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A; Map position: X
A; Introns: 80/2; 104
C; Superfamily: ets I
F; 37-115/Domain: ets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: alternative splicing; DNA binding; nucleus; p. F;55-128/Domain: ets RII regulatory region homology <ETR> F;95-128/Region: helix-loop-helix #status predicted F;334-412/Domain: ets DNA-binding domain homology <ETS> F;374-380/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ets-1
C;Superfamily: transcription factor ets; ets DNA-binding
C;Keywords: alternative splicing; DNA binding; nucleus: r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-438 <STI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: S11225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Characterization of Xenopus laevis cDNA clones A; Reference number: S11224; MUID:90384849; PMID:2205841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Stiegler, P.; Wolff, C.M.; Baltzinger, M.; Nucleic Acids Res. 18, 5298, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor ets-1, splice form a - African clawed frog N;Alternate names: transcription factor p54; transforming protein ets-la C;Species: Xenopus laevis (African clawed frog) C;Date: 18-Feb-1994 #sequence_revision 23-May-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: oocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                              119 TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 TINGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSD:||||||:|||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 PSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEG
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PSSNSTSASK------GPMAIALSATGTGQIQLWQFLLELLADAVNAHCIAWEG
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QLDPYQILG
                                            DNMCLGRISRGKLGGQESFESIESHDSCDRLTQSWSSQSSYNSLQRVPSYDSFDSEDYPP
                                                                                                                                EPSFITESYQTLHPISSEELLS----LKYENDYPLGLLRDPLQPESLQGDYFTIKQEVVTP
                                                                                                                                                                          FPN----TSVYPEATQRITTRPDLPYEQ--
                                                                                                                                                                                                                  LAPDFVGDILWEHLEILQKDSKQYQTSEITPAYPESRYTSDYFISYGIEHAQCYPPSEFS
                                                                                                                                                                                                                                                          LTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQN-----SPRLMHARNTGGATFI
                                                                                                                                                                                                                                                                                                    LPYMSSYHGKRYAYKFDFHGIAQALQ-------PHAH-PQKMNFVAPHP-PALPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRLSTSMSSYHSILSSTSSTSSNQIIPPSTATYWSTPQSSL-TYTGMPSSY
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98; Conserv
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ts DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                    ARRSAWTSHSHPTQSKATQPSSS-----
                                                                                                                                                                                                                                                                                                                                                                                                            17.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: 964614;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 444; DB 1;
Pred. No. 9.6e-24;
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Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirtzlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <ETS>
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 438;
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proto-oncogen
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GA-binding protein alpha chain - human RA-binding protein alpha chain - human RA-binding Farabeas: GABPA; nuclear respictive (man) c:pate: 21-Jan-1994 #sequence_revision C:Accession: A48146; A46303; A55903
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Pathway: known to promote transcription of apolipoprotein A-II, cytochroc; Superfamily: transcription factor elg; ets DNA-binding domain homology; C; Keywords: DNA binding; nucleus; transcription factor
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C:Complex: GA-binding protein is a heterotetramer of two alpha
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A;Note: parts of this sequence were determined by protein set R;Virbasius, J.V.; Virbasius, C.A.; Scarpulla, R.C.
Genes Dev. 7, 380-392, 1993
A;Title: Identity of GABP with NRF-2, a multisubunit activate A;Reference number: A46303; MUID:93194058; PMID:8383622
A;Accession: A46303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:GABPA; E4TF1-60; E4TF1A
A;Cross-references: GDB:138476; OMIM:600609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: cDNA cloning of transcription factor E4TF1 subunits with A; Reference number: A48146; MUID:93180783; PMID:8441384 A; Accession: A48146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Watanabe, H.; Sawada, J.; Yano, K.; Yamaguchi, K.; Goto, M.; Handa, Mol. Cell. Biol. 13, 1385-1391, 1993
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F;322-400/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cardot, P.; Pastier, D.; Lacorte, J.M.; Mangeney, M.; Zannis, V.I.; Biochemistry 33, 12139–12148, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 237-248; 429-448 < VIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA; protein A; Residues: 1-454 <WAT>
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KATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCI
                                                                                       KALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQS
                                                                                                                                                                         VDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSD-----DVD
                                                                                                                                IDLTTL-NISGRELCSLNQEDFFQRVP--RGEILWSHLELLRKYVLASQEQQMNEIVTID
                                                                                                                                                                                                                     KHITTISDETSEQVTRWAAALEGYRKEQERLGIPYDPIQWSTDQVLHWVVWVMKEFSMTD
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26-34,'A',36,'X',38,'X',40-46;151-165;167-174;350-359
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                                                                                                                                                                                                                                                                                                     17.1%; Score 443.5; DB 1; 33.0%; Pred. No. 1.1e-23; wismatches 94;
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A40858
GA-binding protein alpha chain - mouse
GA-binding protein alpha chain - mouse
N;Alternate names: GABPA; nuclear respiratory factor-2 alpha chain; transcription
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1992 #sequence_revision 23-May-1997 #text_change 16-Jul-1999
C;Accession: A40858
C;Accession: A40858
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Science 253, 789-792, 1991
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A;Accession: A40858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA; protein A;Residues: 1-454 <LAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 DRSLFDQG-----VKTDGTVQLSVQVISYQGMEPKL---NILEIVKTAETVEVVIDPD- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parts of this sequence
                                                                KWGQRKNKPTMNYEKLSRALRYYYDGDMICKVQ-GKRFVYKFVCDLKTLIGYSAAELNRL
                                                                                                                                                                                                                                                         TSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNER------
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                                                                                                                                                                       ILGPTSSRLANPG-----SGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVAR
                                                                                                                                                                                                                     -ASVPPAT-----
                                                                                                                                                                                                                                                                                                       RVP--RGEILWSHLELLRKYVLASQEQQMNEIVTIDQPVQIIP
                                                                                                                                                                                                                                                                                                                                              LTPSYNADILLSHLHYLRETPLPHLTSD-----DVDKALQNSPRLMHARNTGGATFIFPN
                                                                                                                                                                                                                                                                                                                                                                                            RKEQERLGIPYDPIRWSTDQVLHWVVWVMKEFSMTDIDLTTL-NISGRELCSLNQEDFFQ
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Search completed: November 9, 2002, 16:54:39 Job time: 32.3864 secs

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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Copyright (c) 1993 - 2002 Compus
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FLII_HOMAN
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GABA_HUMAN
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               RESULT 1

ERG_CHICK

ID ERG_CHICK

ID ERG_CHICK

AC Q99837;

DT 15-DEC-1998 (
DT 16-OCT-2001 (
REG Gallus gallus occurria;
OC Gallus.
OC Gallus.
OC RATChosauria;
OC GALLUS.
OC RATCHOSAURIA

RT PROSOGETHAL

RT PROSOGETHAL

RT PROSOGETHAL

CC -1- FUNCTION
CC -1- FUNCTION
CC -1- SIMILARI
CC -1- SUBCELLU
CC -1- SUBCELLU
CC -1- FUNCTION
CC -1- FUN
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InterPro; IPRO02341; HSF_ETS.
InterPro; IPRO023118; SAM_PNT.
InterPro; IPRO03118; SAM_PNT.
InterPro; IPRO03118; Ets; 1.
InterPro; IPRO0178; Ets; 1.
InterPro; IPRO0454; ETS_DANIN.
INTERPROSITE; PRO0454; ETS_DOMAIN.
INTERPROSITE; PS00345; ETS_DOMAIN.
INTERPROSITE; PS00345; ETS_DOMAIN.
INTERPROSITE; PS00345; ETS_DOMAIN.
INTERPROSITE; PS00346; ETS_DOMAIN.
INTERPROSITE; PS00346
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"Mesodermal expression of the chicken erg gene associated with
"mesodermal expression and cartilage differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precartilaginous condensation and cartilage differ Mech. Dev. 50:17-28(1995).

-I- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR.
-I- SUBCELLULAR LOCATION: Nuclear IN MESODERM- AND FISSUE SPECIFICITY: EXPRESSED IN MESODERM- AND EXTENT, IN ECTODERM-DERIVED TISSUES.
-I- SIMILARITY: BELONGS TO THE ETS FAMILY.
-I- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X77159; CAA54404.1;
HSSP; Q01543; 1FLI.
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MEDLINE=95329425; PubMed=7605748;
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                                                                                                  Transcription
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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ETV1_HUMAN
ETV1_MOUSE
ERM_HUMAN
ETV2_MOUSE
ETV4_MOUSE
ETV4_MOUSE
ELK4_MOUSE
ELK4_MOUSE
ELK4_HUMAN
ELK1_HUMAN
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Best Local Similarity
Matches 458; Conserv
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM ERG-2).
MEDILINE-87263429; PubMed-3299708;
RAO V.N., Papas T.S., Shyam E., Reddy P.;
"erg, a human ets-related gene on chromosome polyadenylation, and translation.";
Science 237:635-639(1987).
                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM ERG-1).
MEDLINE-87317608; PubMed=3476934;
Reddy E.S.P., Rao V.N., Papas T.S.;
"The erg gene: a human gene related to the ets oncogene.
Proc. Natl. Acad. Sci. U.S.A. 84:6131-6135(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERG_HUMAN P11308;
Dunn T., Praissman L., Hagag N., Viola M.V.; "ERG gene is translocated in an Ewing's sarc Cancer Genet. Cytogenet. 76:19-22(1994).
                                                                  CHROMOSOMAL TRANSLOCATION.
MEDLINE=94356859; PubMed=8076344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUL-1989 (Rel. 11, Last
16-OCT-2001 (Rel. 40, Last
Transcriptional regulator E
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-i- FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR (BY SIM
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; ERG-1 AND ERG-
ARE PRODUCED BY ALTERNATIVE SPLICING.
DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML)
BY A CHROMOSOMAL TRANSLOCATION T(16;21)(P11;Q22)
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Papas T.S., Seth A.;
"The ERGB/F11-1 gene: isolation and characterization of of the family of human ETS transcription factors."; cell Growth Differ. 3:705-713(1992).
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                   Biochim. [6]
                                                                                                                   TISSUE-Blood;
MEDLINE-93176799; PubMed-8439553;
Menuw., Denny C., Raskind
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[2]
                                                                                                                                                                                                              Cancer
[5]
                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-93007976; PubMed=1394211;
Prasad D.D., Rao V.N., Reddy E.S.;
"Structure and expression of human
Cancer Res. 52:5833-5837(1992).
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MEDLINE=93075640; PubMed=1445800;
Watson D.K., Smyth F.E., Thompson
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE=92396239; F
  SEQUENCE
                                                                             Beck E., Klemsz M.J.;
"Human FLI-1 localizes
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PRINTS; PRO0454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM\_PNT; 1. Pfam; PF00178; Ets; 1. Pfam; PF02198; SAM\_PNT; 1.

PS00345; PS00346;

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EMBL; AY029368; AAK50443.1; -.
EMBL; BC001670; AAH01670.1; -.
EMBL; BC0010115; AAH10115.1; -.
EMBL; Y17293; CAA76731.1; -.
EMBL; D38408; BAA07463.1; ALT_TE
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TRANSFAC; T02066; -.
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-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98426231; PubMed=9751743; Zucman-Rossi J., Legoix P., Victor "Chromosome translocation based on tumors.";
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email to license@isb-sib.ch).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ
                                                                                                                                                                                                                 GIYPN---TRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                            TSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TINERRYIVPADPILMSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMIKDDFQR
                                                                                                                                                                                             GIYPNPNVPRHPNTHVPSHLGSYY
                                                                                                                                                                                                                                                                                                 NMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQA
                                                                                                                                                                                                                                                                                                                                                                                         PPARVTIKMECNPNQVNGSRNSPDDCSVÄKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM
                                                                                                                                                                                                                                                                LQP----
                                                                                                                                                                                                                                                                                     NMNYDKLSRALRYYDKNIMTKV--
                                                                                                                                                                                                                                                                                                                               TSSRLANPGSGQIQLWQFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKP
                                                                                                                                                                                                                                                                                                                                                                           DQSSRLSVKEDPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGP
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTLYNTEVLLSHLSYLRESSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                           LTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPDYGQPHKINPLPPQQEWINQ}
                                                                                                                                                                                                                                        LQPHPTESSMYKYPSDISYMPSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PVRVNVKREY--DHMNGSRESPVDCSVSKCSKLVGGGESNPMNYNSYMDEKNGPPPPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50061; ETS_DOMAIN_3; 1.
ption regulation; Activator; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
77
130
133
323
426
452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                              (Mouse).
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
361
76
                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.3%;
                                                                                                                                                                                                                                                             ----HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGLAGERA (IN ISOFORM 2).
E > V (IN REF. 5).
MISSING (IN REF. 5).
P -> A (IN REF. 5).
W -> V (IN REF. 5).
E -> Q (IN REF. 4 AND 5).
MISSING (IN REF. 5).
MISSING (IN REF. 5).
W, 9CZNAEEAF683F3FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.905; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETS-DOMAIN.
MDGTIKEALSVVSDDQSLFDSAYGAAAHLPKADMTASGSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1482;
Pred. No. 1
                                                                                                                                                                                              452
                                                                                                                                                                                                                   478
                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POINTED
                                                                                                                                       452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9e-96;
les 80;
                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                               factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein;
translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                               (Retrovira)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5).
                       Euteleosto ; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                       -LAYNTTSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452;
                       leostomi;
inae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        428
                                                                                                                                                                                                                                                             457
                                                                                                                                                                                                                                                                                    368
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                                                                                                                                                                                                                                                                                                                                                     357
                                                                                                                                                                                                                                                                                                                                                                            268
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                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PF00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-siborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sarcoma, encodes a transcriptional activator with DNA-binding specificities distinct from other Ets family members."; Oncogene 8:1621-1630(1993).

-i- EUNCTION: SEQUENCE SPECIFIC TRANSCRIPTIONAL ACTIVATOR. RECOGNIZES THE DNA SEQUENCE 5'C[CA]GGAAGT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59421; CAA42055.1;
PIR; S17403; S17403.
HSSP; Q01543; 1FLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE=93275657; PubMed=8502483;
Zhang L., Lemarchandel V., Romeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Spleen;
STRAIN-BALB/C; TISSUE-Spleen;
MEDLINE-91257578; PubMed-2044959;
MEDLINE-91257578; PubMed-2044959;
MEDLINE-91257578; PubMed-2044959;
MEDLINE-91257578; Detwin K., Bernstein A.;
METYTHROLEUKemia induction by Friend murine leukemia insertional activation of a new member of the ets gen closely linked to C-ets-1.";
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                                                                                        Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000418;
InterPro; IPR002341;
InterPro; IPR003118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T01408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

SUBCELULAR LOCATION: Nuclear.

ITISSUE SPECIFICITY: EXPRESSED IN BOTH HEMATOPOIETIC NONHEMATOPOIETIC TISSUES.

INDUCTION: SPECIFICALLY UP-REGULATED IN LEUKEMIC CLC F-MULV INSERTIONS UP-STREAM OF THE FLI-1 LOCUS.

IDISEASE: INVOLVED IN ERYTHROLEUKEMIA INDUCTION BY FF LEUKEMIA VIRUS (F-MULV).

SIMILARITY: BELONGS TO THE ETS FAMILY.

SIMILARITY: CONTAINS 1 POINTED (PMT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes Dev. [2]
                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang L., Lem
Bernstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The Fli-1 proto-oncogene, involved in erythroleukemia
                                                                                                                                                                                                              Local
61
                                            60
                                                                                                                                         ш
                                                                                   MGI:95554; Fli1
- PVRVNVKREY - - DHMNGSRESPVDCSVSKCNKLVGGGEANPMNYNSYMDEKNGPPPPNM
                                       PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKH-IPPPNM 118
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                 114
281
452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5:908-918(1991).
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                 198
361
51002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSF_ETS.
                                                                                                                                                                                                              57.0%;
57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ets.
                                                                                                                                                                                                                                                                                   WW;
                                                                                                                                                                                           53;
                                                                                                                                                                                      Score 1474; E
Pred. No. 7e-9
63; Mismatches
                                                                                                                                                                                                                                                                                 POINTED.
ETS-DOMAIN.
; 1F9A06C6893FE2AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activator with DNA-binding Ets family members.";
                                                                                                                                                                                                                                                                                                                                                                            DNA-binding;
                                                                                                                                                                                                              7e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ben-David
                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                     Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y.,
                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
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                                                                                                                                                                                   Gaps
                                                                                                                                       59
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TRANSFAC; T02067; -.
InterPro; IPR000418; Ets.
InterPro; IPR0002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
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P41157:
01-FEB-1995
01-FEB-1995
16-OCT-2001
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the Euro
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94206844; PubMed=815576;
Meyer D., Wolff C.M., Stiegler P., Sen
Befort J.J., Remy P.;
"X1-fil, the Xenopus homologue of the
embryogenesis in a restricted pattern
                                                                                                                       EMBL; X66979; CAA47389.1;
HSSP; Q01543; 1FLI.
                                                                                                                                                                                                                                                                                                                                                                                          +
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retroviral integration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458
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                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ifted and this statement is not removed. Usage by and for continue to the statement is not removed.
                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOUS SIMILARITY: BELONGS TO THE ETS FAMILY.

SIMILARITY: CONTAINS 1 POINTED (PMT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIYPNPSVPRHPNTHVPSHLGSYY
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Best Local
SEQUENCE FROM N.A.
MEDLINE-94019387; PubMed-841
Rivera R.R., Stuiver M.H., S
"Ets proteins: new factors t
gene expression.";
gene expression.";
13:7163-716
-i- FUNCTION: ACTS AS A TRAN
                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
[1]
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P81270;
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SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00346; ETS_DOMAIN_3; 1.
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Transcriptional regulator
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           13:7163-7169(1993)
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ver M.H., Steenbergen R.,
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36, Last sequence up
37, Last annotation
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Rodentia;
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Sciurognathi; Muridae,
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Q01414;
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Qi S., Chen Z.Q., Papas T.S., Lau
"The sea urchin erg homolog defin
      DNA
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                                     domain
                                                                                                                                                                                                                 NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                       Eukaryota; N
Echinoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSVYPEATQRITTRPDLPYEQARRSAWTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVSPHPPALPVTSSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIAQALQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKSKPNMNYDKLSRALRYYYDKNIMTKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSVYPEATQRITTRPDLPYEPPRRSAWTGHSHLTPQSKAAQPSPSAVPKTEDQRPQLDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGAAFIFPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00178; Ets; 1.
; SM00413; ETS; 1.
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Q01543; 1FLI.
   3:127-129(1992)
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IPR002341;
                                                                                                                                                                                                                                                                       Metazoa; Echino
Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
272
272 i
                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 31, Created)
(Rel. 31, Last seq
(Rel. 37, Last ann
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BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erg.
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272
                                                                                                                                                                                                                                                                                                   us (Sea urchin).
Echinodermata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.4%;
82.9%;
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HSF_ETS.
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                                                                                                                                                                                                                                                                                                                                                                                          c sequence update)
c annotation updat
ERG homolog (Frag
                                                                                                                                                                                                                                                                             Echinacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1253.5;
Pred. No. 9.2e
1; Mismatches
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                                                           Lautenberger J.
fines a highly
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                                                                                                                                                                                                                                                                                                      Eleutherozoa;
                                                                                                                                                                                                                                                                          Temnopleuroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                          update)
(Fragment).
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  (See http://www.isb-sib.ch/announce/
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A.;
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                                                                                                                                                                                                                                                                                                   Echinozoa;
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                                                                                                                                                                                                                                                                       Toxopneustidae;
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                                                        erg-specific
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Best Local
                                                                                                                                                                                                                                                                                                                   ETS6_DROME S
P29776; Q9VPQ9;
01-APR-1993 (Rel
MEDINE-2016(06; pubMed=10731132; MEDINE-2016(06; pubMed=10731132; MEDINE-2016(06); Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.
                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-binding protein D-ETS-6.
ETS21C OR ETS-6 OR CG2914.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Archropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 DROME
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                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000418;
InterPro; IPR002341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ACTS AS A TRANSCRIPTIONAL ACTIVATOR. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGOIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M81067; AAA68905.1; -. Q01543; IFLI.
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173 AA;
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                                                                                                                                                                                                                                                                                                                                                STANDARD;
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19690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%;
61.9%;
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HSF_ETS.
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Pred. No. 4.5e
l3; Mismatches
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; F85D496DD58A8F3D CRC64;
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.5e-35;
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                                   G.L.
                                                                            S.N.,
                                 B.D.,
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RA Durbin K.J., Evangelisa C.C., Ferrac C., Ferriera S., Dunkov B.C., Dunn P. Ra Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Kanshi D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Ra Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C., Ra Hashi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ra McIntov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra McIntov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Nalson D.R., Nixon K., Nusskern D.R., Pacleb J.M., Ra Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Rainert K., Remington K.A., Stauders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T., Ra Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T., Ra Shue B.C., Wassarman D.A., Weinstock G.M., Weissenbach J., Yang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Yeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Firthe genome sequence of Drosophila melanogaster.";

"The genome sequence of Drosophila melanogaster.";
 Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1
                                                                                                                                                                                                                                                                                          EMBL;
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Dev.
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Dodson
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Cherry
                              SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
SMAST; SM00251; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                    HSSP; Q01543; 1FLI.
FlyBase; FBgn0005660;
InterPro; IPR000418; 1
                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
DNA-binding;
                                                                                                                                                                    InterPro; IPR002341;
InterPro; IPR003118;
                                                                                                                                                                                                                                                        EMBL; M88475; AAA28452.1;
PIR; S28823; S28823.
                                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92249640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 235-352 FROM N.A.,
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solation and characterization of f
ets-related DNA binding domain.";
v. Biol 151:176-191(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz Pablos B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.
                                                                                                                                                                                                                                                                                                                            send
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TISSUE SPECIFICITY: EMBRYONIC VENTRAL NERVOUS
NEURONS IN EACH THORACIC SEGMENT.
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a D., Botchan M.R., Bouck
                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
 : Nuclear
255 33
                                                                                                                                                                                                                                                                                            AAF51484.1;
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ETS3_DROME STANDARD,

P29774; Q9VRU5;

01-APR-1993 (Rel. 25, Created)

1-CCT-2001 (Rel. 40, Last sequence upda

T 15-UN-2002 (Rel. 41, Last annotation up

T 15-TUN-2002 (Rel. 41, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 166;
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          MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Man K.H., Babayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brack
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                            SEQUENCE FROM
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SOFT WE DESCRIBE THE DESCRIPTION OF THE PROPERTY OF THE PROPER
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Query Match
Best Local S
Matches 108
                                                                                                                                                                                                                           PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003563; AAF50
EMBL; M88473; AAA2845
PIR; S28820; S28820.
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-i- TISSUE SPECIFICITY: EMBRYONIC VENTRAL NERVOUS SYSTEM,
THE THORACIC THAN ABDOMINAL SEGMENTS.
-i- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT
-i- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                   DNA-binding; Nuclear DNA_BIND 11 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0005658; Ets65A
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"Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain.";
Dev. Biol. 151:176-191(1992).
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STRAIN=Canton-S; TISSUE=Larva;
MEDLINE=92249640; PubMed=1577186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier E Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devis P. Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz
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                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS
                                                                                                                                                                                                                                                                                                                                                                                                             PF00178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q01543;
                                  Similarity
                                                                                                                                    184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8-69 FROM N.A.,
   Conservative
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Botchan M.R., Bouck J., Brokstein P., Brottier
Busam D.A., Butler H., Cadieu E., Center A., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA28450.2;
                                                                                                                                                                                                                                                                                                                                                                                                             Ets;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF50695.1; -.
                                                                                                                                    20721 MW;
                                  19.4%;
                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION,
                                  Pred. No.
                                                                  Score 502.5; DB 1;
                                                                                                                                                                       ETS-DOMAIN
                                                                                                                                 3F8AD7D0C88BCE8B CRC64;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE
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                                  .7e-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
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                                                                  Length 184;
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
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49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zheng L.,
Smith H.O.,
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RESULT 10
ELG_DROME
RA Adams M.D., Cedniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards G., Zhang Q., Chen L.X., RA George R.A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ray Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Harnis J.F., Aghayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Benos P.V., Berman B.D., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Belcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J., Harvey D., Heimann T.J., Hernandez J.R., Houck J., Andrews D., Heit Y., Levitsky A.A., Li J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D., Ra Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Shee H., Standaling A.C., Stappleton M., Strong R., Sunth T.,
                           ALD PART REPORTED TO THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-binding protein D-ELG.
ETS97D OR ELG OR CG6338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "molecular characterization and structural organization of D-elg, an ets proto-oncogene-related gene of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandbulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93096481; PubMed=1461651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 7:2471-2478(1992).
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REAL REAL PROPERTY OF THE PROP
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                                                                        Matches
                                                                                                                                  Query Match
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InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR0023418; SAM_PNT;
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00198; SAM_PNT; 1.
PRINTS; PR00454; ETSD0MAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
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EMBL; AE003758; AAF56638.1; -.
EMBL; X58481; CAA41390.1; ALT_
EMBL; M88471; AAC34199.1; -.
PIR; S24300; S24300.
PIR; S24300; S24300.
PIR; S26822; S26822.
PIR; S37616; S37616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-9249 DUN, KATIM F.D., Thummel C.S.;
Chen T., Bunting M., Karim F.D., Thummel C.S.;
"Isolation and characterization of five Drosophila genes that encount of the property of the control of the property of the control of the property of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS5061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                   DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE.
STRAIN-Canton-S; TISSUE-Larva;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 298-449 FROM N.A., DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pribyl L.J., Watson D.K., Schulz R.A., "D-elg, a member of the Drosophila ets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 323-463 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91319397;
                                                                    Local Sir
hes 113;
      73
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SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT LEVELS DURING LARVAL DEVELOPMENT.
NQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000422;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T02085;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                       Nuclear
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                                                                                                                                                                                                                                   269
425
454
                                                                                                                                                                                                    52658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Ets.
; HSF_ETS.
; SAM_PNT.
                                                                                                17.6%;
                                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ALT_INIT.
                                                                                                                                                                                                       ₩.
                                                                    60;
                                                                                                                                                                                             POINTED.
ETS-DOMAIN.
L -> V (IN REF. 2).
; 258A1F7C8DF427A2 CRC64;
                                                                                                Score 455;
Pred. No. 1
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                                                                 Mismatches
                                                DB 1,
1.2e-24;
95;
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gene 1
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family:
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                                                                                                                               Length 464
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                                                                 Indels
----PNMTTNERRV 125
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                                                                 84;
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                                                          Gaps
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RESULT 11
ET1A_XENLA
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                                                                            InterPro;
InterPro;
                                                                                                                                                                 the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Use entitles requires a license agreement (See httors and an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ET1A_XENLA
P18755;
                                                                                                                           EMBL; X52692; CAA369
PIR; S11225; S11225.
                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; C-ETS-1A (SHOWN ETS-1A; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                   Stiegler P., Wolff C.M., Baltzinger M., Hirzlin J.,
Meyer D., Ghysdael J., Stehelin D., Befort N., Remy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordat;
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 18:5298-5298(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-ETS-1A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                       TRANSFAC; T02040;
                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
-1- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                        *Characterization of Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90384849;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNYEKLSRALRYYYDGDMISKV-------SGKRFAYKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---IGSGNNGQVQLWQFTLEILTDCEHTDVIEWVGTEGEFKLTDPDRVARLWGEKKNKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATQRITTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIFWTHLQLLKECNEVSVVHKRAEEQRKPKQ--PRIMSANSISTNSGGSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIPEAANEWTHAHVTYWLEWAVKQFELVGINMSDWQ-MNGQELCAMTHEEFNQKLPRDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- EQRI----- MRKSYQSVKSSDSVESTTSSMNPSNYTT--
                                                                                                                     P14921;
                                                                            IPR000418;
IPR002341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus.
                                                                                                                                            CAA36919.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2205841;
                                                           HSF_ETS.
SAM_PNT.
                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                   Befort N., Remy P.;
cDNA clones of the c-ets-1 proto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM\_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.

InterPro;

IPR003118;

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RESULT 12
GABA_H
ID GABA_H
AC Q06546
AC Q06546
DT 01-FEB
DT 16-OCT
GN E4TF1A
OS Homo S
OC E4KATY
OC MAMMA1
OX NCBL_T
RN [1]
RP SEQUEN
RX MEDLIN
RA HANDA
RT "CDNA
RT MOLOCA
RT MOLOCA
RT MEDLIN
RA GUGNEJ
RT nuclea.
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Best Local S
Matches 115
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95097980; PubMed-7799916;
Gugneja S., Virbasius J.V., Scarpilla R.C.;
Gugneja S., Virbasius J.V., Scarpilla R.C.;
"Four structurally distinct, non-DNA-binding subunits nuclear respiratory factor 2 share a conserved transcrinction domain.";
                                                                                                                                                         MEDLINE-93180783; PubMed-8441384;
                                                                                                                                                                                                                                                                              Q06546; Q12939;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GA binding protein alpha chain (GABP-alpha subunit) (Triffactor E4TF1-60) (Nuclear respiratory factor-2 subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DNA_BIND
MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                      NCBI_TaxID=9606
                                                                                                                                                                                                                                                                        E4TF1A OR GABPA
                                                                                                                                                                                                                                                                                                                                                                      GABA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                      403
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                                                                                                                           cloning on motifs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKEQQRLGIPIDPREWTDMHVREWVSWAVNEFTLKGVDFQKF-CMSGAALCALGKECFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMPSHKSKGTFKDYVRDRAELNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLDPYQILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNMCLGRISRGKLGGQESFESIESHDSCDRLTQSWSSQSSYNSLQRVPSYDSFDSEDYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPSFITESYQTLHPISSEELLS----LKYENDYPLGLLRDPLQPESLQGDYFTIKQEVVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTPSYNADILLSHLHYLRETPLPHLTSDDVDKALQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT--
                                                                                                                                                     H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00345;
PS00346;
PS50061;
                                                                                                             Biol. 13:1385-1391(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Nuclear
51 13
332 41
153 15
279 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                      of transcription
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50267
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ETS-DOMAIN.
EHOSPHORYLATION (BY CAMK) (POTE PHOSPHORYLATION (BY CAMK) (POTE PHOSPHORYLATION (BY CAMK) (POTE PHOSPHORYLATION (BY CAMK)).
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Catarrhini;
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                                                                                                                                                                 K.-I.,
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                                                                                                                                                                                                                                                                                                                                                                   454
                                                                                                                                       E4TF1
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Best Local S
Matches 112
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HSSP;
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SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01390; -. Genew; HGNC:4071; GABPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -No1.
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Transcription
DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002341; HSF InterPro; IPR003118; SAM_E Pfam; PF00178; Ets; 1. Pfam; PF02198; SAM_E PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 600609;
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FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INFRICH REPEATS (A REPEATS). NECESSARY FOR THE ADENOVIRUS E4 GENE.
SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO SUBCELLULAR LOCATION: NUClear.
SIMILARITY: BELONGS TO THE ETS FAMILY.
SIMILARITY: CONTAINS 1 POINTED (PMT) DOMAIN.
FVCDLKTLIGYSAAELNRLVTECEQKKLA-KMQLHGIAQ
                       YPSDLPYMSSYHG
                                                       TWEGTINGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYK
                                                                                         KALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPYEQARRSAWTSHSHPTQS
                                                                                                                                                                                  IDLTTL-NISGRELCSLNQEDFFQRVP--RGEILWSHLELLRKYVLASQEQQMNEIVTID
                                            SWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDGDMICKVQ-GKRFVYK
                                                                                                    KATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSNSNCI
                                                                                                                                                                                                          VDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSD-----DVD
                                                                                                                                                                                                                                KHITTISDETSEQVTRWAAALEGYRKEQERLGIPYDPIQWSTDQVLHWVVWVMKEFSMTD
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Q00422;
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                            PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
PS50061; ETS_DOMAIN_3;
                                                                                                                                       ----IIPASVQSAT---
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320
289
440
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170 251
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328 290
440 440
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AAA65706.1; -.
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33.0%;
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                                                                                                                                                                                                                                                                                                                            MW;
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                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                           Score 443.5; DB 1;
Pred. No. 7.3e-24;
Pred. No. 7.3e-24;
                                                                                                                                                                                                                                                                                                                        ETS-DOMAIN.
SS -> RC (IN REF. 2).
A -> V (IN REF. 2).
; laF2ABBBC79191DD CRC64;
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               KRYAYKFDFHGIAQ
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                                                                                                                                                                                                                                                                                                                                                                                  Nuclear
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436
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RESULT 13
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Best Local
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Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
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PDB; 1AWC; 18-MAR-98.
TRANSFAC; T00298; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.
MEDLINE=91343912; PubMed=1876836;
MEDLINE=91343912; PubMed=1876836;
MEDLINE=91343912; PubMed=1876836;
MEDLINE=91343912; PubMed=1876836;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q00422;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                       PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
Transcription regulation; DNA-binding; Nuclear DOMAIN 170 251 POINTED.
DNA_BIND 320 400 ETS_DOMAIN.
DNA_BIND 320 400 ETS_DOMAIN.
SEQUENCE 454 AA; 51363 MW; 76BC47EB2F56JAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T01402; -. MGD; MGI:95610; Gabpa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The structure of GABPalpha/beta: heterodimer bound to DNA."; Science 279:1037-1041(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MEDILINE=90128030; PubMed=9461436; Batchelor A.H., Piper D.E., de la Brousse Wolberger C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA binding protein alpha chain (GABP-alpha subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000418;
InterPro; IPR002341;
InterPro; IPR003118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamarco K., Thompson C.C., Byers B.P., Walton E.M.,
"Identification of Ets-and notch-related subunits i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090
                          75
                                                                       78
                                                                                                                         15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICH REPEATS (GA REPEATS).
SUBUNIT: HETEROTETRAMER OF TWO
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: UBIQUITOUS. SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN
VNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNER---
                                                                       DRSLFDQG------VKTDGTVQLSVQVISYQGMEPKL---NILEIVKTAETVEVVIDPD-
                                                                                                                      DOSLFECAYGSPHLAKTEMTASSSSEYGOTSKMSPRVPQQDWLSQPPARVTIKMECNPNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M74515; AAA53030.1;
                                                                                                                                                                           126;
                                                                                                                                                                                                  Similarity
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                                17.1%;
28.6%;
                                                                                                                                                                           68;
                                                                                                                                                                     Score 441.5;
Pred. No. 1e-2
68; Mismatches
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ETS-DOMAIN.
76BC47EB2F563AAD
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                                                                                                                                                                                                                                                                            CRC64;
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n GA binding
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                                                                                                                                                                                                                                                                                                                                                      3D-structure
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                                                                                                                            TRANSFAC;
InterPro;
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel.
01-MAR-1989 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                   or send
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-1- SIMILARITY: BELONGS TO THE ETS
-1- SIMILARITY: CONTAINS 1 POINTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification in chickens of an evolutionarily conserved ets-2 gene (c-ets-2) encoding nuclear proteins related to t products of the c-ets proto-oncogene."; EMBO J. 7:697-705(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-ETS-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boulukos K.E., Pognonec P.,
Stehelin D., Ghysdael J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=F1broblast;
MEDLINE=88283637; PubMed=3293999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                 InterPro;
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                                                                                                                                                                               S00386; TVCHE2.; P14921; 2STT.
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                                                                                                                                                                                                                                  X07202; CAA30178.1;
                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
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                                                                        IPR002341;
IPR003118;
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(PNT) DOMAIN.
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Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM\_PNT; 1.
Pfam; PF02494; ETSDOMAIN

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P14921;
01-APR-1990
01-APR-1990
16-OCT-2001
                                                                                                                                                                                                                                                       MEDLINE=89083219; PubMed=3060801; Reddy E.S.P., Rao V.N.; "Structure, expression and alternative proto-oncodene.";
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01-APR-1990 (Rel. 14, Last sequents of the correct of the created of the correct of the correct of the correct of the correct of the created of the correct of the correct
                                                                Watson D.K., McWilliams M.J., Lapis P., Lautenberger J.A., Schweinfest C.W., Papas T.S.; "Mammalian ets-1 and ets-2 genes encode highly conserved proteins."; Proc. Natl. Acad. Sci. U.S.A. 85:7862-7866(1988).
                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89042086; PubMed=2847145;
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  STRUCTURE BY NMR OF 320-415.
MEDLINE-96097120; PubMed-8521493.
                                                                                                                                                                                                                           Oncogene
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Mammalia; Eutheria;
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
Proto-oncogene; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SM00251;
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18; Conservative
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SAM_PNT; 1.
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54540 MW;
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Primates;
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31.1%;
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annotation update)
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4; Mismatches 10
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ETS-DOMAIN.
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Best Local
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EMBL; X14798; CAA32903.1; -
EMBL; X04101; AAA52410.1; -
PIR; A32066; TVHUET
PIR; S10086; S10086
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SEQUENCE
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MOD_RES
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Werner M.H., Clore G.M., Fisher C.L., Fisher R.J., Trishiloach J., Gronenborn A.M.;
"The solution structure of the human ETS1-DNA complex mode of binding and true side chain intercalation.";
Cell 83:761-771(1995).
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002341; HSF_E
InterPro; IPR003118; SAM_P
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1
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MIM; 164720; -.
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PDB; 2STW; 12-MAR-97
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                         PROSITE; PS50061; ETS_DOMAIN_3; 1.
Proto-oncogene; DNA-binding; Nuclear
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-1- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: ETS IS RESPONSIBLE FOR ERYTHROBLAST AND FIBROBLAST TRANSFORMATION. THE JUXTAPOSITION OF THE INTERFERON AND C-ETS-1 PROTO-ONCOGENE MAY BE INVOLVED IN THE PATHOGENESIS OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION.
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                                                                                                                                    TINERRVIVPADPILMSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMIKDDFQR 178
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                      SEPSFITESYQTLHPISSEELLSLKYENDYPSVILRDPLQTDTLQNDYFAIKQEVVTPDN
                                                IFPN----TSVYPEATQRI----
                                                                       LAPDFVGDILWEHLEILQKEDVKPYQVNGVNPAYPESRYTSDYFISYGIEHAQCVPPSEF
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                                                                                                                      TKEQQRLGIPKDPRQWTETHVRDWVMWAVNEFSLKGVDFQKF-CMNGAALCALGKDCFLE 115
                                                                                                                                                                         114;
                                                                                                                                                                                    Similarity
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PS00346; ETS_DOMAIN_2;
TTRPDLPYEQARRS--AWTSHSHPTQSKATQPSSSTVPK---
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441 AA;
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HSF_ETS.
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POINTED (PNT) DOMAIN.
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Pred. No. 1.
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ch com	406	391	356	331	296	285	236
Search completed: November 9, 2002, 16:51:18 Job time : 22.0958 secs	406AGKRYVYRF 414	391 PSDLPYMSSYHGKRYAYKF 409	356 WTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKT 405	331 WEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHPPESSMYKY 390	296 PNHKPKGTFKDYVRDRADLNKDKPVIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFIS 355	285	236 MCMGRTSRGKLGGQDSFESIESYDSCDRLTQSWSSQSSENSLQRVPSYDSFDSEDYPAAL 295
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Result
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re greater than or equal to the score of the result being pu
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O80uu0 gallus gall
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O91xv5 rattus norv
O920k9 mus musculu
O9w6z9 xenopus lae
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O93425 coturnix co
O99u61 brachydanio
O95t62 drosophila
O95t62 drosophila
O95t60 hediste div
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2 drosophila
0 hediste div
5 caenorhabdi
          perinereis
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6 bra	057586	13	494	10.9	282	45
homo	Q16031	4	64	10.9	283	44
7	Q8TAC8	4	143	11.0	284	43
Q9puq1 brachydanio	Q9PUQ1	13	491	11.0	284.5	42
Q27378 caenorhabdi	Q27378	υı	441	11.0	285	41
Q90zs9 brachydanio	Q90ZS9	13	444	11.1	288.5	40
	095238	4	335	11.2	290.5	39
dros	Q9VC38	υī	613	11.2	291	38
mus musc	Q9WTP3	1	325	11.2	291	37
093322 xenopus lae	093322	13	477	11.4	295.5	36
gallus g	9MHX6	13	477	11.4	296	S
6 xenopu	Q9W696	<u>1</u> 3	477	11.5	297	34
	Q967C5	<sub>5</sub>	115	11.6	300	33
hedis	Q95ZE1	σ	161	12.1	312	32
homo	Q9BX30	4	512	12.3	318	3
mus	Q8R4Z4	11	513	12.4	320	30
mus musc	Q9QZW1	11	513	12.4	320	29
	Q91744	13	268	12.6	325	28
Q9yhu5 fugu rubrip	Q9YHU5	13	440	15.4	398.5	27
Q9i9e8 brachydanio	Q919E8	13	455	5	406.5	26
6 mus	Q99K36	11	468	•	421	25
	062803	σ	426	σ.	424	24
Q26645 strongyloce	Q26645	ر.	559	σ.	426.5	23
Q921d8 mus musculu	Q921D8	11	393	9	430.5	22
8 mus	844160	Ľ	351	•	437.5	21
062804 ovis aries	062804	σ	336	•	443	20
caenorh	Q18579	υı	208	•	445	19
d	070132	11	340	18.2	472	18
Q8qzw2 mus musculu	Q8QZW2	11	237		472	17

## ALIGNMENTS

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RESULT 1

Q920KT
ID 9920
AC 9920
AC 9920
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Best Local Sim
Matches 431;
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OZAWA R., NOGUCH! H., Taylor T.D., Takeda T.,

PMUS musculus Erg mRNA.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBC
EMBL; AB073080; BAB69950.1; -.

MGD; MGI:95415; Erg.

InterPro; IPR000418; Ets.

InterPro; IPR003141; HSF_ETS.

InterPro; IPR00318; SAM_PNT.

Pfam; PF00178; Ets; 1.

Pfam; PF00178; Ets; 1.

PROSITE; PS00345; ETS_DOMAIN_1; UNKNOWN_1.

PROSITE; PS00346; ETS_DOMAIN_2; UNKNOWN_1.

PROSITE; PS00346; ETS_DOMAIN_3; 1.

PROSITE; PS00361; ETS_DOMAIN_3; 1.

PROSITE; PS0061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q920K7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q920K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                ARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTN 121
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                        88.6%; Score 2293.5; DB 11
86.5%; Pred. No. 7e-171;
Live 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                 BF1ADF00A4772F75 CRC64;
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                          The role of ERG (etz related gene) in cartilage development of the cartilage 9:841-847(2001).

REMBL; ANO65661; AAL40889.1; ...

R InterPro; IPR000418; Ets.

R InterPro; IPR002341; HSF_ETS.

R InterPro; IPR001660; SAM.

R InterPro; IPR003118; SAM_PNT.

R InterPro; IPR003118; SAM_PNT.

R Pfam; PF00178; Ets; 1.

R Pfam; PF00178; Ets; 1.

R Pfam; PF002198; SAM_PNT; 1.

R PRINTS; PR00454; ETS: 0.

R SMART; SM00413; ETS; 1.

R SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Erg isoform C-1-1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chord
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                                                                                                                                                                                                        J. Cell
[2]
                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-20351415; PubMed-10893254;
Iwamoto M., Higuchi Y., Koyama E., Enomoto-Iwamoto M., Kurisu K.,
Yeh H., Abrams W.R., Rosenbloom J., Pacifici M.;
"Transcription factor ERG variants and functional diversification chondrocytes during limb long bone development.";
J. Cell Biol. 150:27-40(2000).
PROSITE; PS00345;
PROSITE; PS00346;
PROSITE; PS50061;
                                                                                                                                                              Yeh H., Rosenbloom
                                                                                                                                                                                  MEDLINE=21535378;
                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                           Archosauria;
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                            M., Higuchi Y., Enomoto-Iwa
Rosenbloom J., Pacifici M.;
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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; ETS_DOMAIN_1;
; ETS_DOMAIN_2;
; ETS_DOMAIN_3;
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Neognathae;
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Last sequence upon Last annotation
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Galliformes; Phasianidae; Phasiani
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; UNKNOWN_
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Best Local
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"Mus musculus Erg mRNA.";
Submitted (OCT-2001) to the EMBL/G
EMBL; AB073079; BAB69949.1; -.
MGD; MGI:95415; Erg.
InterPro; IPR000418; Ets.
InterPro; IPR003418; EAM_PNT.
InterPro; IPR003118; SAM_PNT.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PROSITE; PS00346; ETS_DOMAIN_1; UN
PROSITE; PS00346; ETS_DOMAIN_2; UN
PROSITE; PS00346; ETS_DOMAIN_3; 1.
SEQUENCE 463 AA; 51971 MW; 510
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       Q920K8
Q920K8;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
Erg protein.
ERG.
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SEQUENCE
                                                                                                                                                                                                                                                                  Ozawa
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451 AA; 51002 MW;
                                                                                                                                                                                                                                                              Noguchi H.,
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1 (TrEMBLrel.
2 (TrEMBLrel.
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Rodentia;
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86.3%;
                                                                                                                                                                                                                                                  Taylor A.";
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Last sequence update)
Last annotation updat
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Pred. No. 1.7e-168;
0; Mismatches 1; ]
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3E6C48BCA615AA31 CRC64;
                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                              .D.,
                      UNKNOWN_1.
UNKNOWN_1.
  510D2BB76663D4A4 CRC64;
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Best Loc
Matches
   InterPro; IPRO00418; Ets.
InterPro; IPRO02341; HSF_ETS.
InterPro; IPRO023418; SAM_PNT.
InterPro; IPRO03118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF002198; SAM_PNT; 1.
PF1NTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                 Q9W700;
Q9W700;
01-NOV-1999
01-NOV-1999
01-DEC-2001
Erg protein.
                                                                                                                                                      Dev.
                                                                                                                                                                  plead
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20099678; PubMed=10633861;
Baltzinger M., Mager-Heckel A.M.,
                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                        EMBL; ĀJ224125; CAE
HSSP; Q01543; IFLI.
                                                                                                                                                                                                                                               Xenopodinae; Xen
NCBI_TaxID=8355;
[1]
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for a role in endothelial cell differentiation.
Dyn. 216:420-433(1999).
AJ224125; CAB46566.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Pred. No. 1.6e-162;
11; Mismatches 11;
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Last
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                                                                                                                                                                                                 Remy P.;
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; Pipidae;
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Best Local s
Matches 409
protein.";

Submitted (AUG-1999) to the EMBL/C
EMBL; AB031088; BAB62744.1; -.

InterPro; IPR000418; Ets.

InterPro; IPR002341; HSF_ETS.

InterPro; IPR003118; SAM_PNT.

Pfam; PF00178; Ets; 1.

Pfam; PF00198; SAM_PNT; 1.

Pfam; PF02198; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Vascular endothelial cell specific protein 14.
                                                                                                                                                                                                                                                                                                                                                 Q91XV5;
                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                    Aoki T., Toyoda "Identification
                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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409; Conserv
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                    H., Nishimoto S., Tawara J., Ukai of VESP14,a vascular endothelial (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478
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Rodentia;
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83.1%;
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Pred. No. 5.1e
L9; Mismatches
                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                             Sciurognathi;
                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
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1e-162;
                                                                                                                                                                                                                                                                                       on update)
                                                                                                                                                                                                                               Muridae;
                                                                                                        databases
                                                                                                                                    i Y.,
cell
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473 466

420

Murinae;

Rattus

Komurasaki specific

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PROSITE;
PROSITE;
PROSITE;
SEQUENCE
ILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITT
                                                                                                                                                                              VPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNAD
                                                                                                                                                                                                                      KMECNPSQVNGSRSSPDDCSIGKGSKMGGGSDNVGMNYGSYIEEKHISPPNMTTNERRVI
                                                                                                                                                                                                                                  KMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNERRVI
                                                                                                                                                                                                                                                                          EALSVVSEDQSLFECTYGTPHLTKTEMTASSSSDYGQTSKMSPRVPQQDWLSQPPSRVTI
                                                                                                                                                                                                                                                                                        EALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQPPARVTI
                                                                                                            ILLSHLHYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGASFIFPNSSVYQDANQRIPS
                                                                                                                                                                 VPADPTLWSTDHVRQWLEWAIKEYGLPDVDVLLFQNIDGKELCKMTKEDFHRLTPSYNAD
                                                                                                                                                                                                                                                                                                                                                                               PS00345; 1
PS00346; 1
PS50061; 1
485 AA;
                                                                                                                                                                                                                                                                                                                                                                               ETS_DOMAIN_1;
ETS_DOMAIN_2;
ETS_DOMAIN_3;
A; 54804 MW; F
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2; 1.
3; 1.
F87BF36DAFBA279F (
                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                              Indels
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SQ
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Best Local S
Matches 412
Ozawa R., Noguchi H., Taylor T.D., Takeda T.,
"Mus musculus Erg mRNA.";
Submitted (OCT-2001) to the EMBL/GenBank/DDB.
EMBL; AB073078; BAB69948.1; -.
MGD; MGI:95415; Erg.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
PROSITE; PS00346; ETS_DOMAIN_1; UNKNOWN_1.
PROSITE; PS00346; ETS_DOMAIN_3; 1.
                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; K
NCBI_TaxID=10090;
                                                                                                                                                                              Q920K9
Q920K9;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
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ETS_DOMAIN_3; 1.
51382 MW; B7E2A1564F8
                                                                                                                                      Chordata;
Rodentia;
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); Mismatches
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Pred. No. 7.36
                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
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Murinae; Mus
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Best Local s
Matches 408
               SEQUENCE FROM N.A.

MEDLINE-20099678; PubMed-10633861;

MEDLINE-20099678; PubMed-10633861;

A Baltzinger M., Mager-Heckel A.M., Remy P.;

A Long Expression and pattern and overexpression during plead for a role in endothelial cell differentiation.";

Dev. Dpv. 216:420-433(1999).

EMBL; AUZ24116; CAB46567.1; -.

HSSP; Q01543; IFLI.

InterPro; IPR002418; Ets.

InterPro; IPR002341; HSF_ETS.

InterPro; IPR002341; HSF_ETS.

InterPro; IPR003118; SAM_PNT.

Pfam; PP02198; SAM_PNT; 1.

PRINTS; PR0454; ETSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W6Z9;
Q9W6Z9;
01-NOV-1999
01-NOV-1999
01-DEC-2001
Erg protein.
                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;

Xenopodinae; Xenopus.

NCBI_TaxID=8355;
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408; Conservative
  SM00413;
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Pred. No. 1.1e-159;
1; Mismatches 14;
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Q1-MAY-2000 (Tx)
Q1-MAY-2000 (Tx)
Q1-DEC-2001 (Tx)
F11-1 protein.
FLI1 OR FLI-1.
embryos.
Mech. De
EMBL; AJ
HSSP; Q0
ZFIN; ZD
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PROSITE;
PROSITE;
PROSITE;
                                                                          SEQUENCE FROM N.A.

MEDLINE-20108585; PubMed-10640707;

Brown L.A., Rodaway A.R., Schilling T.F., Jowett
Patient R.K., Sharrocks A.D.;

"Insights into early vasculogenesis revealed by
domain transcription factor Fli-1 in wild-type a
                                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              443
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AJ249590; CAB56832.1
Q01543; 1FLI.
ZDB-GENE-980526-426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SM00251; SAM_PNT;
TE; PS00345; ETS_DOM
TE; PS00346; ETS_DOM
TE; PS50061; ETS_DOM
NCE 456 AA; 51482
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0 (TrEMBLrel. 1
1 (TrEMBLrel.
                                               90:237-252(2000)
                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                              CAB56832.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ETS_DOMAIN_1;
; ETS_DOMAIN_2;
; ETS_DOMAIN_3;
A; 51482 MW; F
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77.5%;
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b; Pred. No. 3.3e
19; Mismatches
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                                                                                                                                                                                                                                                                                                          Created)
Last sequence
Last annotation
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; Craniata;
Teleostei;
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.ta; Vertebrata; Euteleostomi;
.ta; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                              451
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1.3e-149;
les 23; ]
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                                                                                                                              Jowett
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                                                                              y expression
and mutant :
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ID 093425
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DT 00
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Best Local Sin
Matches 289;
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Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
Pfam; PF02198; SAM_PNT; 1.
SMART; SM00413; ETS; 1.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1
PROSITE; PS00346; ETS_DOMAIN_2; 1
PROSITE; PS00361; ETS_DOMAIN_3; 1
SEQUENCE 451 AA; 50655 MM; F4:
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093425;
01-NOV-1998
01-NOV-1998
01-JUN-2001
FLI transcri
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InterPro;
  SEQUENCE FROM N.A.
MEDLINE-98358003; PubMed-9694627;
Mager A.M., Graphin-Botton A., Ladjali
Stiegler P., Bonnin M.A., Remy P.;
                                                                                                                                             Eukaryota; Metazoa;
Archosauria; Aves;
                                                                                     NCBI_TaxID=93934;
[1]
                                                                                                                                                                                        Coturnix
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NOV-1998 (TrEMBLrel. 08,
JUN-2001 (TrEMBLrel. 17,
transcription factor.
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MDGTIKEALSVVSEDQSLFEPPYAAAAPLPKTDMTASGTQDYGQTHKINPIPPQQEWINQ
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                                                                                                                                         coturnix japonica (Japanese quail).
a; Metazoa; Chordata; Craniata; Vertebrata; Eute
ria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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57.6%;
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HSF_ETS.
SAM_PNT.
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                                                                                                                                                                                                                                                Created)
Last sequence
Last annotation
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Pred. No. 2.7e
3; Mismatches
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                       Meyer
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                       D.,
                       Wolff C.
                                                                                                                                                                Euteleostomi;
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RESULT
Q9PUL6
ID Q9PUL6
AC Q9
AC Q9
DT 01
DT 01
DT 01
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GN F1
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GN F1
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Best Local (
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EMBL; Y14773; CAA75077.1; --
EMBL; Y14774; CAA75077.1; --
EMBL; Y14774; CAA75078.1; --
EMBL; Y14774; CAA75078.1; --
HSSP; Q01543; IFLI.
InterPro; IPR00418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
SMART; SM00413; ETS; 1.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT.
                                                              Q9PUL6; PRELIMINARY;
Q9PUL6;
01-MAY-2000 (TrEMBLrel. 13, (
01-MAY-2000 (TrEMBLrel. 13, 1
01-DEC-2001 (TrEMBLrel. 19, I
Fill protein (Fragment).
          Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
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                                                                                                                                                                                             IYPNPNVPRHPNAHVSPHLGSYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ
                                                                                                                                                                                                                                               QPHPTESSMYKYPSDLSYMPSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASPYWTSPAGS
                                                                                                                                                                                                                                                                                                                 MNYDKLSRALRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKEDFHGIAQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMV-SSSDNVGMNYGSYMEEKHIPPPNM
                                                                                                                                                                                                                        IYPN---TRLPAAHMPSHLGTYY 478
                                                                                                                                                                                                                                                                            QP-----
                                                                                                                                                                                                                                                                                                      MNYDKLSRALRYYDKNIMTKV--
                                                                                                                                                                                                                                                                                                                                                       SSRLANPGSGQIQLWQFLLELLSDSSNASCITWEGTNGEFKMTDPDEVARRWGERKSKPN
                                                                                                                                                                                                                                                                                                                                                                                                            EASSRLATKEGPPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.3%;
57.1%;
                                                                                                                                                                                                                                                              -----HAHPQKMNEVAPHPPALPVTSSSFFAAPNPYWNSPTGG
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                                                                                                                                                                                                                                                                                                                                                                                                           -----AGTQNVNKT---TEQQRPQPDPYQILGPT
          Teleostei;
                                                                            Last sequence up
                                                                                                      Created)
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3; Mismatches
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                                                                                                                                PRT;
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              danio).
ta; Vertebrata; Euteleostomi;
ta; Vertebrata; Euteleostomi;
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            Ostariophysi;
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nes 72;
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                                                                                        update)
                                                                             update)
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mesenchyme.";
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          Cypriniformes;
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A Detrich H.W., Vail B., Huber T.L., Paw B., Brownlie A.J., Oates A.C.,
A Fritz A., Gates M.A., Amores A., Bahary N., Talbot W.S., Her H.,
A Beier D.R., Postlethwait J.H., Zon L.I.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR177538; AAR01966.1; -.
BR MSSP; Q01543; 1FLI.
DR FIN; ZDB-GENN-980526-426; flil.
InterPro; IPR002418; Ets.
R InterPro; IPR002141; HSE_ETS.
BR InterPro; IPR002141; HSE_ETS.
DR InterPro; IPR002141; HSE_ETS.
DR InterPro; IPR003118; Eds; 1.
Pfam; PF02198; EAM_PNT.
DR Pfam; PF02198; EAM_PNT.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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SEQUENCE
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PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson M.A., Ransom D.G., Pratt S.J., MacLennan H., Kier Detrich H.W.I.I.I., Vail B., Huber T.L., Paw B., Brownlie Oates A.C., Fritz A., Gates M.A., Amores A., Bahary N., Ta Her H., Beier D.R., Postlethwait J.H., Zon L.I.; "The cloche and spadetail genes differentially affect hema and vasculogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE=98294174; Pubmed=9630750;
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                         421
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                      vasculogenesis.";
. Biol. 197:248-269(1998).
                                                                                                                                               NQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNERRVIVPADPT 132
ELPYVPSYHAHQQKVNFVSPHPPSMPVTSSNFFGPTTPYWSSP
                                                          DKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP-----
                                                                                              NYLRES - - -
                                                                                                                                                                                                                 HYLRETPLPHLTSDDVDKALQNSPRLMHARNTGGATFIFPNTSVYPEATQRITTRPDLPY
                                                                                                                                                                                                                                                    LWSPDHVRQWLDWAIKEYGLQEIDTAMFHSTDGKELCKMSKDDFLRLTSVYNTEVLLSHL
                                                                                                                                                                                                                                                                 LWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHL
                                                                                                                                                                                                                                                                                                        DHINGSRESPYDCSYGKCNKMYGGTEASQMNYTGYMDEKCAPPPNMTTNERRYIYPADPS
                                                                                                                                                                                                                                                                                                                                                       EDQSLFEPPYAAAAPLPKTDMTASGTQDYGQTHKINPIPPQQEWINQ-PVRVNVKREY--
                                                                                                                                                                                                                                                                                                                                                                                                           259;
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414 AA;
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                      -HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSP
                                                                                                                                                                                                    -----SSSISYNTPSHADQSPRLAAKDDASY
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Pred. No. 1.4e
50; Mismatches
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                                              HGKRYAYKIDFHGIAQALQPHPTESTMYKYPS
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1.4e-96;
hes 82;
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Talbot W.S.
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PROSITE; PS00346; ETS_DOMAIN_3;
PROSITE; PS50061; ETS_DOMAIN_3;
SEQUENCE 476 AA; 51917 MW; F
  Q95T62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00178; Ets; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
Ewings sarcoma_EWS-F111 (type 1) oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BZD1;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                            YGSPHLAKTEMT---ASSSSEYGQTSKMSPRVPQQDWLSQPPARVTIKM--ECNPNQVNG
                                                                                                                       HPNTHVPSHLGSYY
                                                                                                                                                                       LPAAHMPSHLGTYY 478
                                                                                                                                                                                                                                                                                                                      LRYYDKNIMTKV----
                                                                                                                                                                                                                                                                                                                                          LRYYYDKNIMTKVHPPESSMYKYPSDLPYMSSYHGKRYAYKFDFHGIAQALQP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGQP----TDVSYTQAQTTATYGQTAYATS-----YGQPPTGYTTPTAPQAYSQPVQG
                                                                                                                                                                                                                     YKYPSDISYMPSYHAHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS-QYSQ-QSSSYGQQSPPL--
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                                                                                                                                                                                                                                               -----HAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN---TR
  PRELIMINARY;
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Pred. No. 1.5e-56;
6; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GGAQTISKNTEQRPQPDPYQILGPTSSRLANPGS
  PRT;
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  257
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Q95ZED ID Q95ZE AC Q95ZED DT Q1-DE DT Q1-DE DT Q1-MAD DE Erg p GN ERG. OS Hedis OC Eukar OC Phyll OX NCBL RN [1] RP SEQUE RL SUDmi
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Best Local S
Matches 139
                                                                                                                                                                                                                                                      Q95ZE0;
Q95ZE0;
01-DEC-2001
01-DEC-2001
01-MAR-2002
Bocquet B. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00178; Ets; 1.
PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00345; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
SEQUENCE 257 AA; 28700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY060316; AAL25355.1; -.

ElyBase; EBgn0005658; Ets65A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
Stapleton "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95T62;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                      Eukaryota; Metazoa; Ar
Phyllodocida; Hediste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Eterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                NCBI_TaxID=126592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH18452p.
ETS65A OR CG7018.
                                                STRAIN-DIVERSICOLOR;
                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                         Hediste
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InterPro; IPR002341; HSF_ETS.
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mes 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSASIFPSAASWGNWGSPATNLYQPHSMSHVTPSHVAPHLSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRSTGS----FSNFSM------LFADSSYKSSWGSHS-STQSQGY--SSNALG
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                                                                                                                                                                 Annelida;
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49.1%;
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Last sequence up
Last annotation
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Pred. No. 3.3e
31; Mismatches
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Last sequence update)
Last annotation updat
                                                                                                                                                              Polychaeta;
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                                                                                                                                                              Palpata;
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                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253
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Matches 103
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Thesis (2000), Department of Biologie Animale
Villeneuve d'Ascq, France.
EMBL; AJ311813; CAC44038.1; -.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
PROSITE; PS00345; ETS_DOMAIN_1; UNKNOWN_1.
PROSITE; PS00346; ETS_DOMAIN_3; 1.
               "Direct Submission.";
Submitted (SEP-2001) to the ENEME: U39470; AAC71120.1; -.
HSSP: Q01543; 1FLI.
InterPro: IPRO00418; Ets.
InterPro: IPRO02341; HSF_ETS.
Pfam; PF00178; Ets; 1.
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PROSITE;
PROSITE;
NON_TER
NON_TER
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 41.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q22355
Q22355;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae; NCBI_TaxID=6239;
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SEQUENCE FROM N.A.
                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                  Stellyes L.;
                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. investigating biology. The C. elegan Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T08H4.3
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PRINTS;
                                                                                                                                                                      Waterston
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                                                                                                                                                                                                                                                                            sequence of C.
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164
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18775
                                                                                                                                                                                                                                                        elegans
) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nematoda;
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Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                            EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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Pred. No. 5.3
                                                                                                                                                                                                                                                                                                                                                                                                          elegans
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing
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Best Local S
Matches 133
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NON_TER
SEQUENCE
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"Isolation of members of ets gene family in polychaete annelids.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ278692; CAB99437.1; -.
HSSP; Q01543; IFII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00413; ETS; 1.
PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00345; ETS_DOMAIN_2;
PROSITE; PS00361; ETS_DOMAIN_3;
Hypothetical protein.
SEQUENCE 377 AA; 41466 MW; I
                                                                                                                                                                                                                              PRINTS; PR00454; ETS;
SMART; SM00413; ETS;
PROSITE; PS50061; ET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perinereis cultrifera.
Eukaryota; Metazoa; Annelida; Polychaeta;
Phyllodocida; Nereididae; Perinereis.
NCBI_TaxID=59559;
                                                                                                                                                                                                                                                                                             Pfam; PF00178; Ets;
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InterPro; IPR002341;
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160 /
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16; Mismatches
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THIS PAGE BLANK (USPTO)

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Command line parameters:

-MODEL-frame+_pln.model -DEV=xlp
-Q-/Cgn2_1/USPTO_Spool_VG09902772/runat_07112002_134033_9031/app_query.fasta_1.1294
-DB-GenEmb1 -QFWT-fastap -SUFFIX-rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09902772_@CGN_1_1_3441_@runat_07112002_134033_9031 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOF-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Ygapop 10.0 , X
Fgapop 6.0 , E
Delop 6.0 , I
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29: em_vi:*
30: em_htg_inv:*
31: em_htg_other:*
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33: em_htg_pin:*
34: em_htg_other:*
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36: em_htg_other:*
36: em_htg_other:*
40: em_htgo_nus:*
40: em_htgo_nus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Query Match Length DB

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Direct Submission
Submitted (17-JAN-1994) M. Duterque-Coquillaud,
Oncologie Moleculaire, Institut Pasteur, 1 rue (
Lille, FRANCE
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Phasianinae; Gallus.
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GIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNP
YWNSFTGGIVNNTRLPARHMPSHLGTYY"
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63. .1499
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PD 23-MAR-1999

PF 29-MAX-1998 JP 1998166076

PR 18-JUN-1997 US

PR 18-JUN-1997 US

PI ROZENBUROOM,

PI HELENA E

PC C12M15/09,A61K48/00,C07K14/465,C07K16/18,C12Q:

PC C12P21/02,

PC C12P21/08,C12N15/00,A61K37/02

CC Topology: Linear:

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FT SOURCE 1.1528
                                   HisAlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThr
CysAlaTyrGlySerProHisLeuAlaLysThrGluMetThrAlaSerSerSerSerGlu
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Location/Qualifiers
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Direct Submission
Submitted (16-OCT-2001)
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YAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVSPHPPALPVTSS
SFFASBNPYNNSPTGGTYPNTELPASHMPSHLGTYY"
06 a 608 c 545 g 450 t
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148. .1608
                                                                                                                                                           variant 3"
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/db_xref="taxon:10090"
/chromosome="16"
/clone="Erg-3"
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/note="homolog
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                                   GGCCACAGCCACCTCACCCCTCAGTCCAAAGCTGCTCAGCCATCTCCCCTCTGCAGTGCCC
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Iwamoto,M., Higuchl,Y., Enomoto-Iwamoto,M., Kurisu,K.,
Yeh,H., Rosenbloom,J. and Pacifici,M.
The role of ERG (ets related gene) in cartilage develop
Osteoarthr. Cartill. 9 Suppl A, S41-S47 (2001)
21535378
                                                                                                                                        Iwamoto,M., Higuchi,Y., Koyama,E., Enomoto-Iwamoto,M.,
Yeh,H., Abrams,W.R., Rosenbloom,J. and Pacifici,M.
Transcription factor ERG variants and functional diver:
chondrocytes during limb long bone development
J. Cell Biol. 150 (1), 27-40 (2000)
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E31253 G::13025685
JP 1999075871-A/1.
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CHUGAI PHARMACEUT CO LTD, HE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
OS Unidentified
PN JP 199075871-A/1
PD 23-MAR-1999
PF 29-MAY-1998 JP 1998166076
PR 18-JUN-1997 US 08/878177,20-JUN-1997 US 60/050297 PI HIROYASU IMAMOTO, YOSHINOBU HIGUCHI, MARIJIO PASHIFIKI, PI JOEL ROZENBUROOM,
PI HELENA E
PC C12N15/09,A61K48/00,C07K14/465,C07K16/18,C12Q1/68//A61K38/0
PC C12P21/02,
CC Strandedness: Single;
CC Topology: Linear;
FH Key
I Location/Qualifiers
FT source

//Organism='Unidentified'.
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Sakaki, Y.
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/db_xref="taxon:9606"
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ERG gene; transcription f
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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National de la Recherche
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Baltzinger, M., Mager-Heckel, A.M. and
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                          /db_xref="STPREMB::Q9W700"
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321. .1778
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/clone_lib="lambda ZAPII"
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de la Recherche Scientifique,
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                                                     ---CCATCAAAAGCATCTCAACCA---TCTACCACAGTTCCCAAAACAGAAGACCCCCAGG
                                                                                  AGGCAAGATTTATCATATGAGCCCTCAAGGAGATCTGCTTGGACAAATCATCCTGCACCA
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                                                                                                                Submitted (12-AUG-1999) Tomomi Aoki, Taisho Pharmaceutica Ltd., Medicinal Research Laboratories, Molecular Biology 1-403, Yoshino-cho, Omiya, Saitama 3308530, Japan (E-mail:s17704@ccm.taisho.co.jp, Tel:048-663-1111,
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vascular endothelial cell specific
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/tissue_type="liver"
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                                       ProSerTyrAsnAlaAspIleLeuLeuSerHisLeuHisTyrLeuArgGluThrProLeu
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                                                                                             CAGTGGCTGGAGTGGACAGTGAAAGAATACGGCCTCCTAGACGTGGACGTCTTATTATTT
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QNIDGKELCKMTKDDPGRLTBSYNADILLSHLHYLRETPLPHLTSDDVDKALQNSPRL
MHARNTDLPYEPPRRSTWTGHSHPTPGSKAAQPSPSTVPKTEDDRPQLDPYQILGPTS
SRLANPGSGQ10LWGFLLELLSDSSNSNCITWBGTNGEFKMTDDEDVARRWGERKSKP
NMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSLYKYPSDLP
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Direct Submission

Direct Submission

Submitted (16-OCT-2001) Masahira Hattori, The Institute of Physical Submitted (16-OCT-2001) Masahira Hattori, The Institute of Physical Submitted (16-OCT-2001), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
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Ozawa, R., Noguchi, H.,
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/note="homolog of
variant 1"
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/db_xref="taxon:10090"
/chromosome="16"
/clone="Erg-1"
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                                                                 HisalaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThr
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Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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GluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeu
                                                                                    SerargAlaLeuArgTyrTyrTyrAspLysAsnIleMetThrLysValHisProProGlu
                                                                                                                GAAGTGGCAAGACGTTGGGGGGAGAGGGAAAAGCAAACCCAACATGAACTATGATAAGCTC
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1 (bases 1 to 3126)

Reddy, E.S., Rao, V.N. and Papas, T.S.
The erg gene: a human gene related to the ets oncogene proc. Natl. Acad. Sci. U.S.A. 84 (17), 6131-6135 (1987)
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1 of 2
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TNGEFKMTDPDEVARRWGERKSKPNMYDKLSRALRYYYDKNIMTKVHGKRYAYKFDF
HGIAQALQPHPDESSLYKYPSDLPYMGSYHAHPQKMNFVAPHPPALPVTSSSFFAAPN
PYWNSPTGGIXTRYTKPTSHPSHLCTYYY"

PYWNSPTGGIXTRYTKPTSHPSHLCTYYY"

722 c 725 g 741 t
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476	GlyGlyIleTyrProAsnThrArgLeuProAlaAlaHisMetProSerHisLeuGlyThr	457	Оу
1217	CCCGTGACATCTTCCAGTTTTTTTGCTGCCCCAAACCCATACTGGAATTCACCAAC	1158	Db
456	LeuProValThrSerSerShePheAlaAlaProAsnProTyrTrpAsnSerProThr	437	Qy
<u> </u>	TGGGCT	1098	Db 2
ت د	HisAlaHisProGlnLvsMetAsnPheValAlaProHisProProAl	N (	۷ پر د
	ACCCCCGGAGTCATCTCTGTACAAGTACCCCTCAGACCTCCCG	1038	밁
420	aLeuGlnPr	417	Qy
1037	CATGGGAAGCCTACGCCTACAGTTCGACTTCCACGGGATCGCCCAG	990	рь
416	yrHisGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGl	397	Qy
989	ACCAAGGT	978	ф
396	tThrLysValHisProProGluSerSerMetTyrLysTyrPro	377	Qy
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376	roAsnMetAsnTyrAspLysLeuSerArgAlaLeuArgTyrTyrTyrAspLysAsnIl	357	Qy
917	GAGTTCAAGATGACGGATCCCGACGAGGTGGCCCGGCGCTGGGGAGAGCGGAAGAGCAAA	858	ДЬ
356	luPheLysMetThrAspProAspGluValAlaArgArgTrpGlyGluArgLysSerI	337	Qy
857	CTGGAGCTCCTGTCGGACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGG	798	dd db
336	uGluLeuLeuSerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGl	317	Qy
797	CAACAAGTAGCCGCCTTGCAAATCCAGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTC	738	ф
316	roThrSerSerArgLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLe	297	Qy
737	TCCACAGTGCCCAAAACTGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCTTGGA	678	дъ
296	ThrValProLysThrGluAspGlnArgProGlnLeuAspProTyrGlnIleLeuGl	277	Qy
677	TCAGCCTGGACCGGTCACGGCCCACGCCCCAGTCGAAAGCTGCTCAACCATCTCCT	618	Db
276	erAlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSe	258	Qy
617		591	dd dd
257	AspLeuProTyrGluGlnAlaArgAr	238	Qy
590	TRANTGCATGCTAGAAACACA	570	ф
237	uMetHisAlaArgAsnThr	218	Qy
569	CCTCTTCCACATTTGACTTCAGATGATGTTGATAAA	510	ф
217	hrProLeuProHisLeuThrSerAspAspValAspLysAlaLeuGlnAsnSerProAr	198	Qy
509	GGCTCACCCCCAGCTACAACGCCGACATCCTTCTCTCACATCTCCACTACCTCAGAG	450	ФФ
197	LeuThrProSerTyrAsnAlaAspIleLeuLeuSerHisLeuHisTyrLeuAr	178	Qy
449	TTGTTATTCCAGAACATCGATGGGAAGGAACTGTGCAAGATGACCAAGGACGACGACTTCCAG	390	фd
177	euLeuPheGlnAsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheG	158	Qy
389	CATGTGCGGCAGTGGCTGGAGTGGGCGGTGAAAGAATATGGCCTTCCAGACGTCAACATC	330	Db
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329	ATGACCACGAACGAGCGCAGAGTTATCGTGCCAGCAGATCCTACGCTATGGAGTACAGAC	270	dd dd

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Alignment S
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Query Match:
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Danio rerio 1
AJ249590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1436)
Brown, L.A., Rodaway, A.R., Schilling, T.F., Jowett, T.,
Patient, R.K., and Sharrocks, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to Sharrocks, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insights into early vasculogenesis revealed ETS-domain transcription factor Fli-1 in wil
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-1 gene; Fli-1 proto
to rerio.
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DASYDAVRRTGMSNNHHSGKGSPTVYSGSVSKNEDQDFVQDDFVQILGPTSSTLAAKD
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45. .1400
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mRNA for Fli-1 pr
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                                              /protein_id="aak50443:1"
/db_xref="G1:14017403"
/db_xref="G1:14017403"
/translation="modtikealsvvsddqslfdsaygaaahlpkadmtasgspdygq
/translation="modtikealsvvsddqslfdsaydcsvskcsklvgggesnpmny
NSYMDEKNGPPPPNMTTNERRVIVPADPTLWTQEHVRQWLEWAIKEYSLMEIDTSFFQ
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DPSYDSVRRGAWGNNMNSGLNKSPPLGGAQTISKNTEQRPDPPYQILGPTSSRLANR
GSQQIOLWQFLLELLSDSANASCITWBGTNGEFKMTDDDEVARRWGERKSKPNNYDK
LSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSYH
LSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSYH
                                                                                                                                                                                                                                              /gene="FLI1"
/gene="ETS transcription factor; involved in the
/note="ETS transcription factor; involved in the
pathogenesis of Ewings sarcoma following translocation
with EWS gene on Chromosome 22; may have oncogenic
potential when fused with EWS gene"
                                  AHQQKVNFVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGS
                                                                                                                                                                                                                 /product="friend leukemia integration 1 transcription
                                                                                                                                                                                                                                                                                                                                              /gene="FLI1"
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/db_xref="taxon:9606"
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                                                   ThrValProLysThrGluAspGlnArgProGlnLeuAspProTyrGlnIleLeuGlyPro
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                                                                                                                                AlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGln---ProSerSerSer
                                                                                                                                                                 GluAlaThrGlnArgIleThrThrArgProAspLeuProTyrGluGlnAlaArgArgSer
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                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                       Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, clone MGC:19589 BC010115
     Shevchenko, Y.,
                                                                                                                                                                                                                                                                              Strausberg,R
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                     Contact:
                                                  Gaithersburg, Maryland;
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nisc_mgc@nhgri.nih.gov
Wetherby,K.D., Beckstrom-Sternberg,S
                              http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                          2394 bp mRNA linear PRI 12-JUL-2001 19589 IMAGE:3635042, mRNA, complete cds.
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ThrThrAsnGluArgArgValIleValProAlaAspProThrLeuTrpSerThrAspHis 138

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                                                                 ProProAlaArgValThrIleLysMetGluCysAsnProAsnGlnValAsnGlySerArg 79
                                                                                                                                              GluTyrGlyGlnThrSerLysMetSerProArgValProGlnGlnAspTrpLeuSerGln
    AsnSerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsn 99
                                                                                                                       Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: g Column: 16
This clone was selected for full length sequencing because it for the following selection criteria: matched mRNA gi: 257353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S. Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R. Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
                                            -CCAGTGAGGGTCAACGTCAAGCGGGAGTAT----GACCACATGAATGGATCCAGG
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PHKINFLPPQQEWINQPVRVNVKREYDHMNGSRESPVDCSVSKCSKLYGGGESNPMNY
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GSGQIQLWQFLLELLSDSANASCITWEGTNGEFKNTDPDEVARRWGERKSKPNMNYDK
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/db_xref="taxon:9606"
/clone="MGC:19589 IMAGE:3635042"
/tissue_type="Lymph, Burkitt lymphoma"
/clone_lib="NIH_MGC_8"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Unknown (protein
/protein_id="AAH10115.1"
/db_xref="GI:14603316"
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                                       ProValThrSerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGly
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Db 1410 GGAATCTACCCCAACCCCAACGTCCCCGCCATCCTAACACCCACGTGCCTTCACACTTA 1469

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Search completed: November 9, 2002, 18:55:34 Job time: 3121.42 secs

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Command line parameters:

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-OP-Gygn2_1/USPTO_Spool_VS09902772/runat_07112002_134033_9021/app_query.fasta_1.1294
-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXY=0 -UNITS-bits -START=1 -END=-1 -NATIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCONE=pct -THR_MAX=100 -THR_WIN=0 -NLIGN=15
-NODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NGS_SCONES=0 -NAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AAX26552
ID AAX2 AAX26552 standard; DNA; 1528

AAX26552;

14-JUN-1999 (first entry)

FT OS XXX DNA encoding chicken c-erg protein.

Chicken; C-11 protein; cell calcification inhibiting activity; cell calcification inhibiting agent; c-erg protein; arthritis deformans; ossification; spinal column ligament; ss.

Gallus sp.

Location/Qualifiers 63..1499

CDS

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Alignment Scores:
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18-JUN-1997;
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IT 2 551 AAX26551 standard: DNA: 1447 RP	1443 CCCAATACCAGGCTGCCAGCTGCTCATATGCCTTCCCATCTTGGCACC	roAsnThrArgLeuProAlaAlaHisMetProSerHisLeuGl	441 SerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThr	323 CATGCACACCCCCAGAAGATGAACTTTGTAGCTCCCCATCCCCCTGC	421 H1SA1aH1SPrOGInLySMetAsnPheValAlaProH1SProProAl		401 nisolyμyskigiytkidiythysrneksprnehisolyllekidgi		<b>o</b>	203 CAIGGIAAACGCTAIGCCIACAAATTIGATTI	CO	100	301	361	083 ACAGACCCTGATGAAGTGGCTCGGCGTTGGGGAGAGAGAG	341 ThraspproaspCliValalaargargTrpClvCliargIvec		21 SerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrA	63 CGTCTTGCAAATCCAGGGAGTGGGCAGATACAGCTATGGCAG	gLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGln	903 AAAACAGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCTTGG	hrGluAspGlnArgProGlnLeuAspProTyrGlnIleLeuG	843 ACGAGTCACAGCCATCCCACTCAGTCAAAAGCTACCCAACCATCATC	hrSerHisSerHisProThrGlnSerLysAlaThrGlnProS	783 ACGCAAAGAATAACAAGAAGGCCAGATTTACCTTATGAGCAAGCGAGGAGATC	hrGlnArgIleThrThrArgProAspLeuProTyr	723 GCTAGAAACACAGGAGGAGCCACTTTTATTTTTCCAAATACATCAGTTTA	ArgAsnThrGlyGlyAlaThrPheIlePheProAsnTh	663 CCACATTTGACTTCAGATGATGATAAGGCCTTACAAAACTCTCC	roHisLeuThrSerAspAspValAspLysAlaLeuGlnAsnSe	603 CCGAGCTATAACGCAGATATCCTCCTGTCACACCTACACTACCTCAG	roSerTyrAs	43 CAGA	nAsnIleAs
	TACTA	Tyrī	GlyGlyIleTyr            GAGGCATCTAC	TTTGCCCGTAACC	llllllllllll		nAlaLeuGinPro	BOTTOCIAC		CTCCAGCCT	1	-	ı — ⊢	•		S KO	ATGGGGAGTTCAAGATG	ıeLysMet	TTCCTACTGGAGCTTCTG	luLeuLeu	GACCGACCAGCAGC	lyProThrSerSer	CATCTTCAACAGTGCCC	oĭo	AGCGTGG	rAlaTrp	CCAGAAGCA	rProGluAla	TCCACGGTTAATGCAT		CCTCAGAGAGACTCCTCTT	oLeu	CACG	
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AAX26551 standard;

DNA; 1447

ВP

AAX26551;

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                                                                                                                                                                                                                                                                                                   Sequence 1447 BP;
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 7-8; 15pp; Japanese.
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                                                                                                                                                                                                                                                                                                                        Ligament
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18-JUN-1997;
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                                                                                                                                               TyrGlyGlnThrSerLysMetSerProArgValProGlnGlnAspTrpLeuSerGlnPro
                                                                                                      ProAlaArgValThrIleLysMetGluCysAsnProAsnGlnValAsnGlySerArgAsn
SerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnVal
                     CCGGCCAGAGTTACCATTAAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGAAT
                                                              TATGGGCAAACATCAAAGATGAGCCCGCGCGTTCCCCCAGCAGGACTGGTTATCACAGCCC
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97US-0878177.
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86.35%
86.35%
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Mismatches:
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sAlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuPr	Qy
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401 HisGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnPro 420	Qy
ACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCCTACAT	망
HisProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerT	Qy
ACGCTATGCCTACAAATTTGATTTCCACGGAATCGC!	рь
380 380	Qy
TCAGCCGTGCACTTCGCTACTACTATGACAAAAA	DЬ
yrAspLysLeuSerArgAlaLeuArgTyrTyrTyrAspLysAsnIleMetThrLysVa	γQ
ACAGACCCTGATGAAGTGGCTCGGCGTTGGGGAAGAGGAAAAAGCAAACCTAACATGAAAC 10	당 5
41 ThraspProAspCliValalaardArdTrpClvClimardIvsSerIvsProAspMetase 36	Ş
321 SerAspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMet 340 	DP OA
82 CGTCTTGCAAATCCAGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGG	Ъ
01 ArgLeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLe	Qy
	밁
hrGluAspGlnArgProGlnLeuAspProTyrGlnIleLeuGlyProThrSerSe	Qy
762 ACGAGTCACAGCCATCCCACTCAGAAAAGCTACCCAACCATCATCTTCAACAGTGCCC 821	망
$61\ \ Thr Ser His Ser His Pro Thr Gln Ser Lys Ala Thr Gln Pro Ser Ser Thr Val Fernanda Global Control of the $	Qγ
	Дb
${\tt 41~ThrGlnArgIleThrThrArgProAspLeuProTyrGluGlnAlaArgArgSerAlaTr}$	Qy
57GAGCCACTTTATTTTCCAAATACATCAGTTTACCCAGAAGCA 70	당 4
21 AlaardaanThrGlvGlvAlaThrDheTleDheDrOAsnThrSerValTvrDroGluAla 24	9
56 6	븅
$ 0 1 \   \texttt{ProHisLeuThrSerAspAspValAspLysAlaLeuGlnAsnSerProArgLeuMetHi} \\$	Qγ
	뭥
81 ProSerTvrAsnAlaAspIleLeuLeuSerHisLeuHisTvrLeuArgGluThrProLeu 2	Q
CAGAACATTGATGGGAAAGAGTTGTGTAAAATGACCAAAGATGACTTCCAGAGACTCACG 60	문
61 GlnAsnIleAspGlvLvsGluLeuCvsLvsMetThrLvsAspAspPheGlnArdLeuThr 18	φ
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41 GlnTrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuF	Qy
	Db
21 AsnGluArqArqValIleValProAlaAspProThrLeuTrpSerThrAspHisValArq 1	Qу
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US-09-902-772-4
                                                                          Percent Similarity:
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Plougastel
                                                                                                                                                                                                                                                                                         New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatmen of Ewing sarcoma and melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1362
                                                                                                                                                     Sequence 2938
                                                                                                                                                                                 The probe 11RR1 was used to screen a human marrow cDNA 1 (Clontech cat.# HL1058). The clone BM025 was identified sequenced. It represents the entire coding region togeth 5'- and 3'-UTRs of the Hum-Fli-1 gene.
                                                                                                                                                                                                                                                            Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ews gene; malignant melanoma; hum-fli-1;
primitive peripheral neuroectodermal tumour;
human chromosome 22; ss.
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alignant melanoma; hum-fli-1;
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                                                Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of number of human shear stress response proteins. These are useful diagnosis, treatment and screening of vascular diseases caused by arterioscierosis, including heart failure, post-PTCA restenosis and the protein stream of the protein stream of the protein stream of the protein stream of the protein and coding sequences of the protein stream of the protein and coding sequences of the protein an
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791..850
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/*tag= j
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977..1042
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527..586
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                                                                                      US-09-902-772-4 (1-478) x AAQ50662 (1-1890)
                                                                                                                                                                                                                                The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene have been sequenced (see AAQ50644 and AAQ50662, respectively). The different fusion products which could be formed by fusing exons from the two genes, as happens after specific chromosomal translocations, can be predicted (see AAQ50671-Q50678). The sequences at fusion junctions of other observed translocations are given in AAQ50679-Q50683). NOTE: the 1890 residue sequence AAQ50662 does not appear in the specification; it is a combination of the Hum-Fli-1 cDNA sequence (Fig 7, AAQ50644) and the individual intron sequences
                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma
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P-PSDB; AAR44556.
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Plougastel B, Thomas G,
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                                         GCGGCAGCCCATCTCCCCAAGGCCGACATGACTGCCTCGGGGAGTCCTGACTACGGGCAG
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288 1173	GGAGGGGCACAAACGATCAGTAAGAATACAGAGCAACGGCCCCAGCCAG	1114	db dy
1113	TTTATAGTTCTTTGGAGGCTCACTGCATTTCTTTCCCTCTTGCCACAGGTCCTCCCCCTT	ı G	рb
274	AlaThrGlnPro	271	Qy
1053	GTCAGAAGAGGAGCATGGGCCAATAACATGAATTCTGGCCTCAACAAAAGTAAGT	994	Дb
270	AlaArgArgSerAlaTrpThrSerHisSerHisProThrGlnSerLys	255	Qy
993	TCATTAGACCCTTCTTATGACTCA	934	Db
254	luGln	249	Qy
933	AGTTTGTTCTTTTG	874	Db
248	oGlualaThrGlnargIleThrThrArgPro	235	Qy
873	TCTCAGGTTCACTGCTGGCCTATAATACA	814	ДЬ
234	LyAlaThrPheIlePheProAsnThr	223	Qy
813	CAG	805	Дb
222	SerAspAspValAspLysAlaLeuGlnAsnSerProArgLeuMetHisAlaArg	203	Qy
804	TACAACACGGAAGTGCTGTTGTCACACCTCAGTTACCTCAGGGAAAGTAAGT	745	ФФ
202	AsnAlaAspIleLeuLeuSerHisLeuHisTyrLeuA	183	Qy
744	ATGGATGGCAAGGAACTGTGTAAAATGAACAAGGAGGACTTCCTCCGCGCCACCACCCTC	685	Db
182	leAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThrProSer	163	Qу
684	CTGGAGTGGGCCATAAAGGAGTATAGCTTGATGGAGATCGACACATCCTTTTTCCAGAAC	625	Db
162	luTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuPheGlnAsn	143	Qy
624	TGCAGACCCCACACTGTGGACACAGGAGCATGTGAGGCAATGG	565	Db
142	erThrAspHisValArgGlnTr	129	Qy
564	AATTCGAGAACCAGGCTGCCTGGGCGCCTCCTTGCT	505	Db
128	ArgArgVallleValPro	123	Qy
504	GCCCCCTCCTCCCAACATGACCACCAACGAG	445	Дb
122	lySerTyrMetGluGluLysHisIleProProProAsnMetThrThrAsnGlu	104	Qy
444	GACTGCAGCGTTAGCAAATGCAGCAAGCTGGTGGGCGGAGGCGAGTCCAACCCCATGAAC	385	Db
103	PCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnValGlyMetAsn	84	Qy
384	GCCTGTGCAGGATTGGGCCTTGGGCTTTTGCCCCCCTCACTTTAGGGAGTCTCCGGTG	325	рь
83	ArgAsnSerProAsp	79	Qy
324		271	ф
78	alThrIleLysMetGluCysAsnProAsn	64	Qy
270	CCCCACAAGATCAACCCCCTCCCACACAGCAGGAGTGGATCAATCA	214	Db
63	roProAlaAr	44	Qy

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                                                             09-AUG-2001.
                                                                                                                 disease;
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-----CACGGCAAAAGATATGCTTACAAATTTGACTTCCACGGC
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene, expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                  from human breast
the probes with a
Sequence 567
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 6819; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single
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                                                                                                                                                                                                                                                                                                                                                           acid probes
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2000US-0236359.
2000GB-0024263.
  BP;
  114 A; 124
                                                                                                                                                                                                                                                                                                                  es for measuring gene expression in a sample deri-
and BT 474 cells. The method involves contacting
collection of detectably labelled nucleic acids
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Alignment Scores:

Best Local Similarity: Query Match: 1.78e-57 801.00 78.17% 76.65% 30.95% Gaps: Mismatches: Indels:

US-09-902-772-4 (1-478) × ABA48124 (1-567)

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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                            Human genc
analyzing
                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from hum liver. The single exon nucleic acid probes may be used for p measuring and displaying gene expression in samples derived fetal liver. The present sequence is a single exon nucleic a probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                             Claim
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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cardiovascular disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human heart present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derifrom the human heart via microarrays. By measuring gene expression, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 567
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RESULT 10
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Query Match:
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                       Penn
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26-MAY-2000;
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                         AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr
                                                                   LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSer
                                                                                                                                                                                                                                                                                                                                       SG,
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                                                           CTGACCTCATTAGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCCTGGAGCTCCTGTCG
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                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                              (1-478) x AAK14426
                                                                                                                                                                                                                                                                           SEQ ID NO:
                                                                                                                                                                                                                                                                                                     nucleic
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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Alzheimer's disea
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801.00
78.17%
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samples, which may enable the improved diagnosis and treatment of such as lymphoma, leukaemia and myeloma. The present sequence is the probes of the invention.

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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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AAK40160
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hur bone marrow. They can be used to measure gene expression in bone man
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                               Example 4;
                                               analyzing
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                                                       genome-derived
                                                                                                     MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                 standard;
                                               gene
                               SEQ
                                                                                                                   ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234683.
; 2000US-02346359.
                                                                                                                                                                                                                                           marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
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                                               human bone marrow
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RESULT 12
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                                    Probe; human; mi cervical cancer;
                                                           Probe #10865
       WO200157278-A2
                                                                         12-OCT-2001
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| GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG
                                                                                                                                                                                                                                                              GlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnPro---
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                                           gene expression;
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26-WAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to human single exon nucleic acid
                                                                                                                                                                                                                                         AspSerSerAsnSerAsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThr
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| GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG
                                                                                                                                                                                                                                                                                        GlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnPro---
                                                                                                                                                          AspLysLeuSerArgAlaLeuArgTyrTyrAspLysAsnIleMetThrLysValHis
                                                                                                                                                                                                       AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr
                                             GGGAAGCGCTACGCCTACAAGTTCGACTTCCACGGGATCGCCCAGGCCCTCCAGCCCCAC
                                                                                                                    ProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHis
                                                                                                                                              GATAAGCTCAGCCGCCCCCCCCTTACTACTATGACAAGAACATCATGACCAAGGTC---
                                                                                                                                                                                           CATCCCGACGAGGTGGCCCGGGGGGGGGGGGGGGGGGAGAGCCAAACCCCAACATGAACTAC
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Conservative:
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Best Local S:
Query Match:
DB:
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AAI46176/c
ID AAI461
XX AAI461
XX AAI461
XX Probe;
XW PR 00-AUG
XW 30-JUN
PR 27-SEP;
PR 27-SEP;
PR 21-SEP;
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US-09-902-772-4 (1-478) x AAI46176
                                                                                                       Percent Similarity:
                                                                                                                                                                     Alignment Scores:
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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an placenta -
                                      Length:
Matches:
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302 LeuAlaAsnProGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuGluLeuSer

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RESULT 14
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                   2001-476286/51
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                                                                                          MOLECULAR
                                                      Hanzel
                                                                                                                           ; 2000US-0180312.

2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236839.

2000US-0236339.
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Novel single exon nucleic acid probe used in a human breast -  $\,$ IJ No 6634; English. ç measuring gene expression

The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO probe

Sequence 567 BP; 114 A; 124 0 200 G; 129 H 0 other;

ftp.wipo.int/pub/published\_pct\_sequences.

Best Local Query Match US-09-902-772-4 Percent Similarity: Alignment Scores: ö Similarity: (1-478)1.78e-57 801.00 78.17% 76.65% 30.95% x AAI06643 (1-567)Length:
Matches:
Conservative: Gaps: Mismatches: Indels: 567 151 3 3 40

Ъ Ş 534 302 

321

341

Q 밁 δõ 문 362 414 342 AspSerSerAspSerAspCysIleThrTrpGluGlyThrAspGlyGluPheLysMetThr |||||||||||||||| |GACAGCTCCAACTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACG GATCCCGACGAGGTGGCCCGGCGCTGGGGAGAGCGGAAGAGCAAACCCAACATGAACTAC AspProAspGluValAlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyr 415 381 355 361

δÃ 밁 382 354 ProProGluSerSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHis GATAAGCTCAGCCGCCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTC---AspLysLeuSerArgAlaLeuArgTyrTyrAspLysAsnIleMetThrLysValHis 401 298

294 GlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnPro---GGGAAGCGCTACGCCTACAAGTTCGACTTCCACGGGATCGCCCAGGCCCTCCAGCCCCAC 235

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밁 Q 421 234 CCCCCGGAGTCATCTCTGTACAAGTACCCCTCAGACCTCCCGTACATGGGCTCCTATCAC Н15 421 175

ρy 밁 174 422 AlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeuProValThrSer GCCCACCCACAGAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCCGTGACATCT 441

RESULT 15 ABS14215/c

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ABS14215

standard;

DNA;

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CC The invention relates to a spatially-addressable set of single exon concluded acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 crobes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a croarray comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring sequences of the array; identifying exons in a eukaryotic genome, comprising (c) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, camprising a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, camprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several conficorarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single exon probe; and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases.
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Note: The sequence data for this patent did not form part
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-DB=Issued_Patents_NA -QPMT-fastap -SUFFIX-rni -MINATCH-0.1 -LOOPCL-0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
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## ALIGNMENTS

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; LENGTH: 1528
; TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: chugai seiyaku kabushiki kaisha 5001
CURRENT APPLICATION NUMBER: US/08/878,177
CURRENT FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwamoto et TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes TITLE OF INVENTION: the Proteins
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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TGTGCCTACGGATCGCCCCACCTTGCAAAGACAGAAATGACAGCCTCCTCCTTCCAGTGAA
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Sequence 1, Application US/08878177

Patent No. 6294354

GENERAL INFORMATION:

APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwam
ITILE OF INVENTION: Cell Calcification Suppressing Pro
ITILE OF INVENTION: the Proteins

FILE REFERENCE: chugai seiyaku Kabushiki kaisha 5001

CURRENT APPLICATION NUMBER: US/08/878,177

CURRENT FILING DATE: 1997-06-18

NUMBER OF SEO ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 1447

TYPE: DNA

ORGANISM: C-11 gene, c-erg gene w/ deletion, chicken
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               SerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGlyGlyIleTyr
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                                                                                       Percent Similarity:
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Patent No
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                              NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DISM PC COMPUTED:
COPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text edi
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: 20cman, Jessica
TITLE OF INVENTION: UNCLEDE ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CAN
TITLE OF INVENTION: TRANSLACATIONS AND NUCLEIC ACIDS OF FUSION RESULTING FROM
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR 9:
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/1 FILING DATE: 19-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCI/FR93/00494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associat
STREET: 230 South Fifteenth
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APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitty V.
APPLICANT: Hyodoro, Dmitty J.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-04027
CURRENT APPLICATION NUMBER: US/09/435,335
CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: 09/360,779
EARLIER FILING DATE: 1999-07-26.
NUMBER OF SEQ ID NOS: 23
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rSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerPro
                                                  ACAGGCTTGCCAGCCACCACCCGCGCACGCCCACGCCGCCGCTGCCGCCGCCGCAGCGGC
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рь 99 Оу 45	ACGCCACCGCCGCTGC	1031
Db 1032	CGCCGCCACCGCTGCGCTCTACCCAACCCCGGGCTTGCAGCCCCCCCC	1091
Oy 467 Db 1092	467 -AlaAlaHisMetProSerHisLeuGlyThrTyrTyr 478	
RESULT 6 US-09-34 ; Sequer ; Patent	6 44-579-1 nce 1, Application US/09344579 t No. 6054316 t NO. 6054316	
APPLICA APPLICA TITLE ( FILE RI CURRENT CURRENT CURRENT NUMBER	мирю не:	
S S	LENGTH: 2268 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (291)(1700)	
Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB:	ment Scores:       6.71e-35       Length:       2268         No.:       442.50       Matches:       13         nt Similarity:       39.50%       Conservative:       40         Local Similarity:       30.37%       Mismatches:       108         Local Similarity:       17.10%       Indels:       158         Gaps:       16	
-09-	-772-4 (1-478) x US-09-344-579-1 (1-2268)	1
Oy 12 Db 57	122 GluArgArgVallleValProAlaAspProThrLeuTrpSerThrAspHisValArgGln 141 :::     :::	.41
Oy 14 Db 63	142 TrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuPheGln 161	36
Qy 16 Db 68	2 AsnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThrPro 1 ::::::   :::	.81
Oy 18	82 SerTyrAsnAlaAspIleLeuLeuSerHisLeu	รั มี
Оу 19	ω	6
Db 807		90
Qy 19	7 GluThr 1	.98
Db 86	7 AGCAATACATTAGGTTTTGGCACAGAGCAGGCGCCCCTATGGAATGCAGACACAGAATTAC 9	26
0у 19	9ProLeu-ProHisLeuThrSerAspAspVa 2	808
Db 92	CACCCAGCGTACTCAGCTCT 9	86
. N	8 lAspLysAlaLeuGlnAsnSerProArgLeu	<b>. . . .</b>
Db 98	7 GAGCAGGAGTTTCAGATGTTCCCCAAGTCTCGGCTCAGCTCCGTCAGCGTCACCTGC	1046

atent No. 5734039 GENERAL INFORMATION: APPLICANT: Calabretta, Bruno APPLICANT: Skorski, Tomasz TITLE OF INVENTION: ANTISENSE TITLE OF INVENTION: OLIGONUCLEO NUMBER OF SEQUENCES: 55 CORRESPONDENCE ADDRESS: ADDRESSEE: Seidel, Gonda, Lav STREET: Two Penn Center, Suit CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.	
SULT 7 -08-306-691B-43 Sequence 43. Application US/08306691	
Db 1725GCCCCAGGCTCGTGGGACTGAGTGGGAAGCCCATCCTGACCAGCTGCCT 1772	
Qy 429 eValalaproHisproproAlaLeupro 438	
1674 -GGCGTCCAGCCCGACACGGAGGACTGAGGTCGCCGGGACCACCCTGAGCCG 17	
Qy 416 nAlaLeuGlnProHisAlaHisProGlnLysMetAsnPh 429	
ASPENDENTS LIFE CONTROL OF THE CONTR	
1590TCGGGGAAGCGCTACGTGTACCGCTT 16	
Qy 389 sTyrProSerAspLeuProTyrMetSerSerTyrHisGlyLysArgTyrAlaTyrLysPh 409	
Db 1556 CTACTATTACGACAAGAACATCATCCACAAGACG	
- H	
1496 GTGGGGAAAGAGGAAAATTAAGCCCAAGATGAACTACGAGAAGCTGAGCC	
TrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArg/	
QY 3-29 ETHILIPULUG-TYTHIASHG-LYG-HENDENSMETTHIASBUTTOASBUTTWALALARIGAT 349  1:::	
13/0 INTICAUCIGIUGCAGITICICCIGGAGCIGCIAICAGACAAAICCIGCCAGICAITCAI 14	
309 nIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAsnCysII 329	
Db 1337 ACCTGCAGCTGTGCTGGCCGGCTTCACA	
rSerSerArgLeuAlaAsnPro	
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269 rLvsAlaThrGlnProSerSerSerThrValProLvsThrGluAspGlnArgProGlnLe 289	
VY 201 THE SELECTION OF	
161	
251 oTyrGluGln 260	
Db 1107 CCCAAAGACCACGACTCCCCTGAGAACGGTGCGGACAGCTTCGAGAGCTCAGACTCC 1163	
Qy 231 eProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAspLeuPr 251	
Db 1047 TCTGTCAGTCAGGACTTCCCCAGGCAGCAACTTGAATTTGCTCACCAACAATTCTGGGACT 1106	
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TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5349
TELEFAX: (215) 568-5349
TELEFX: No. 5734039e
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1604 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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FILLING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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684 GATGTGAAACCATATCAAGTTAATGGAGTCAACCCAGCCTATCCAGAATCCCGCTATACC
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
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                                                                                                                                                                                                                                                                                                                                                          AGTTC---TGTATGAATGGAGCAGCCCTCTGCGCCCTGGGTAAAGACTGCTTTCTCGAG
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                                            GCTCCTCTCCCTCAAGTATGAGAATGACTACCCCTCGGTCATTCTCCGAGACCCTCTCCA 922
                                                                                                        TCGGATTACTTCATTAGCTATGGTATTGAGCATGCCCAGTGTGTTCCACCATCGGAGTTC
                                                                                                                                         rGlyGlyAlaThrPheIle-----
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STATE: COUNTR ZIP: COMPUTER MEDIUM COMPUTER SOFTWA: CURRENT APPLIC, APPLIC, APPLIC, APPLIC, APPLIC, APPLIC, APPLIC, APPLIC, ATTORNEY, NAME: REGIST: REGIST REFERE TELECOMM TELEPH	SULT GEN A A T	Qy 390 Db 1494	Qy 370 Db 1463	Qy 350 Db 1403	Qу 330 рь 1343	Qy 310 рь 1283	Qy 290 Db 1223	Oy 285 Db 1163	Qy 277 Db 1103	Qy 258 Db 1043	Qy 249 рь 983	
NY Y: US 11530 READA READA READA TYPE: ETYPE: ATION REATION DATE: FICATION DATE ATION CE/DO UNICAT ONE: X: 51	6251- 9, p 1NFC CANT: OF I OF I OF I SPONI	rProSerAspLeuProTyrMetSerSerTyrHisGlyLysArgTyrAlaTyrLysPhe 409	TTYTTYTASPLYSASNIleMetThrLySValHisProProGluSerSerMetTyrLySTy 390	pGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAlaLeuArgTy 370 	rTrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAlaArgArgTr 350	eGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAsnCysIleTh 330 	PPTOTYTG1nI1eLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGlnI1 310 ::: ::	GCCCAACCACAAGCCCAAGGGCACCTTCAAGGACTATGTGCGGGACCGTGCTGACCTCAA 1222	rThrValProLys 284 :::::: ::: CAGCCTGCAGCGTGTTCCCTATGACAGCTTCGACTCAGAGGACTATCCGGCTGCCCT 1162	-SerAlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSe 277 ::::::	PLEUPTOTYTGluGlnAlaArgArg257 ::::	

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LENGTH: 1604 base pair:
TYPE: nucleic acid
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                                                                         CAGCCTGCAGCGTGTTCCCTCCTATGACAGCTTCGACTCAGAGGACTATCCGGCTGCCCT 1162
                                                                                                  rThrValProLys-----
                                                                                                                          AGAGAGCTACGATAGTTGTGATCGCCTCACCCAGTCCTGGAGCCAGTCATCTTTCAA 1102
                                                                                                                                                 -SerAlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSe
                                                                                                                                                                          CATGTGCATGGGGAGGACCAGTCGTGGTAAACTCGGGGGGCCCAGGACTCTTTTGAAAGCAT 1042
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pProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGlnIl 310
                          GCCCAACCACAAGCCCAAGGGCACCTTCAAGGACTATGTGCGGGACCGTGCTGACCTCAA
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44.21%
30.26%
17.02%
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S	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2667 base pairs	TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300	REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 015280-229000 TRIEGOMMINATION INFORMATION:	ATTORNEY/AGENT INFORMATION: NAME: Garrett-Wackowski, Eugenia	APPLICATION NUMBER: US/08/469,412A FILING DATE: 05-JUN-1995 CLASSIFICATION: 435	SOFTWARE: Patentin I CURRENT APPLICATION DAY		ZIP: 94111-38 COMPUTER READABI	STATE:	ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco	NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:	APPLICANT: Sgouras, TITLE OF INVENTION:	APPLICANT: APPLICANT:		o. 5856125 INFORMATION:	SULT 9 -08-469-412 Sequence 1,	1494	Jy 390 rProSerAspLeuProTyrMetSerSerTyrHisGlyLysArgTyrAlaTyrLysPhe	Db 1463 CTATTACGACAAAAACATCATCCACAAGACA	370	ш	350	27 330 11190100121111ASHOLJOLUCHELIS STECLILIAS PELOAS POLITICALIALI SALGLI 11	200	1 31	Db 1223 TAAGGACAAGCCTGCTGCTGCTGCTGCCTAGCTGGCTACACAGGCAGTGGACCAAT
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Best Local Similarity:
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Patent No. 6194547
GENERAL INFORMATION:
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                             CORRESONDENCE ADDRESS:
CORRESONDENCE Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
CORRESON. Two Embarcadero Center, Eighth Floor
                                                                                       Beal Jr., Gregory J.
Athanasiou, Meropi A.
Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                               APPLICANT: Mavrothalassitis, George
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STREET: Two Embarcadero
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                    Fisher, Robert J.
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SEQUENCE CHARACTERISTICS:
LENGTH: 2667 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                  yrAlaTyrLysPheAspPheHisGlyIleAlaGlnAlaLeuGlnProHis------
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                                                                                                                                                                            roGlySerGlyGlnIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerA
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|TISCCTCAAGGCAGATCCAGCTGTGGCACTTTATCCTGGAGCTGCTGCGGAAGGAGGAGG
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                                                                            erSerMetTyrLysTyrProSerAspLeuProTyrMetSerSerTyrHisG1yLysArgT 405
                                                                                                                                    erArgAlaLeuArgTyrTyrTyrAspLysAsnIleMetThrLysValHisProProGluS
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ACCAGGGCGTCATTGCCTGGCAGGGGGACTACGGGGAATTCGTCATCAAAGACCCTGATG
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LOCATION: 123..1769
LOCATION: 123..1769
OTHER INFORMATION:
Factor) cDNA
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-343-443B-5
Alignment Scores:
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                                                                                                                                                                                                                 TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR
FILING DATE: 19-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: FR 92/
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSE: Weiser & Associates
STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID CO
TITLE OF INVENTION: CHROMOSOME 22 I
TITLE OF INVENTION: TRANSLATIONS AS
TITLE OF INVENTION: TUMORS, AND NUC
TITLE OF INVENTION: TRANSLOCATIONS
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                                                                                                FEATURE
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 328 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                              NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
                                                                            NAME/KEY:
                                                                                                                TOPOLOGY:
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/343,443B FILING DATE: 18-NOV-1994
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                                                                                                                                                                                                                                                      TELEPHONE:
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Peter, Martine
Ploougastel, Beatrice
Thomas, Gilles
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Desmaze, Chantal
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                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                       UMBER: FR 92/06123
20-MAY-1992
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6096542 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
                                                          TELEFAX: (202) 737-3528 INFORMATION FOR SEQ ID NO:
                                                                                     NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                 APPLICATION NUMBER: JP 07-020173
FILING DATE: 08-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/000:
FILING DATE: 09-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             FILING DATE: 07-AUG-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HIGASHINO, Funihiro TITLE OF INVENTION: CANCER CONTROL NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                          SEQUENCE CHARACTERISTICS:
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CITY: Washington
STATE: D.C.
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STRANDEDNESS
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                           LENGTH:
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         nucleic acid
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                             2064 base pairs
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07-AUG-1997
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301.50
79.31%
65.52%
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Matches:
Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                        263
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AACAGGAACAGACGTTCGCCTACGACTCAGATGTCACCGGGTGCGCATCAATGTACC
                                                 ATCCCCAGCAGAGCTTTAAGCAAGAATACCATGATCCCCTGTATGAACAGGCGGGCCAGC 652
                                                                                                                                                                          ePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAspLe 250
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Matches:
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US-09 Patcy GEN AP FI	B 8	Оу	Оy	Оy	Дy	Db Qy	Оу	Дb	Дb	Qy Db	DЬ	Qy	Qy dd
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149-3 3, Application US/0 3, Application US/0 3, Application US/0 2048351 11	rArgLeuProAlaAla 468 :::        GGCTGTTCCCCCTGCC 141	TYTT-	nLysMetAsnPheValAlaP::::   ::::   GAGGACACAGTCCCTTTGTC	AlaTyrLysPheAspPheHis-GlyIleAlaG         :::       :::: GCTCTCAAGGCTGAGTTTGACCGGCCTGTCA-	LysTyrProSe:    :::  AAGTTTGTGTGTGAGCCCGA	ArgTyrTyrTyrAspLysAsnIleMetThrLysValHi           :::                  CGATACTATTATGAGAAAGGCATCATGCAGAAGGTG	ArgTrpGlyGluArgLysSe:       :::   :: CTCTGGGGCATCCAGAAGAA	IleThrTrpGluGlyThrAs:            ATTGCCTGGACGGGCCGGGG	GlnIleGlnLeuTrpGlnPh :::          GCCCTGCAGCTGTGGCAATT	ThrSerSerArgLeuAlaAsnPr            ACATCAAGCAGGAAGGGGTCGGT	AGAAACCTCTGCGACCATTCCC		GluAspGlnArgProGlnLe
9116049A  DEAG IS A TUMOR SUPPRESSOR FOR CANCER US/09/116,049A  17-15  Length: 2064 Matches: 136 Conservative: 41 Mismatches: 141 Indels: 192 Gaps: 17	3	rpasnSerProThrGlyGlyIleTyrProasnTh	nLysMetAsnPheValAlaProHisProProAlaLeuProValThrSerSerSerPhePh ::::	lnAlaLeuGlnProHisAlaHis	LysTyrProSerAspLeuProTyrMetSerSerTyrHisGlyLysArgTy	nIleMetThrLysValHisProProGluSerSerMetTyr 	ArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAlaLeu         :::   ::::	IleThrTrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluValAlaAr	InIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAs 	oglySe -gcatitcgagaggggccgccctaccagcgccc	CCAGATGATGTCTGCGTTGTCCCTGAGAAATTTGAAG		gProGlnLeuAspProTyrGlnIleLeuGlyPro
CELLS		snTh 463 CAGC 1397	hePh 445 :: GGCT 1344	ProG1 425 :: GTGAG 1284	ArgTyr 405     CGTCCA 1248	tTyr 388 :    GTAC 1188	aLeu 368 :    GCTC 1131	aArg 348      CAGG 1071	snCys 328 :: ATTTC 1011	rGly 308      GGGT 951	GGAG 892	297	297 TATG 832

US-09-902-772-4 (1-478) x US-09-116-049-3 (1-2064)

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RESULT 14
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bandma
                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/055,113 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                  TELEX:
                                                   TELEFAX: 650-845-4166
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT12
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290 AspProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGln 309
                                                                                                                                                                                                           230 IlePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAsp 249
                                                                                                                                                                                                                                                                           210 LysalaLeuGlnAsnSerProArgLeuMetHisAlaArgAsnThrGlyGlyAlaThrPhe 229
                                                                                                                                                                                                                                                                                                                                           190 SerHisLeuHisTyrLeuArgGluThrProLeuProHisLeuThrSerAspAspValAsp 209
                                                                                                                                                                                                                                                                                                                                                                           982 GCCATGTCGGAGGAGCAGTTCCGCCAGCGCTCGCCC---CTGGGTGGGGATGTGCTGCAC 1038
                                                                                                                                                                                                                                                                                                                                                                                                     170 LysMetThrLysAspAspPheGlnArgLeuThrProSerTyrAsnAlaAspIleLeuLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 TyrGlyLeuProAspValAspIleLeuLeuPheGlnAsnIleAspGlyLysGluLeuCys 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754 CCC-----GGCGGGCTGACCTTGGAGGAGCACTCGCTGGAGCAGGTGCAGTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GlyMetAsnTyrGlySerTyrMetGluGluLysHisIle-----ProProProAsnMet 118
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                                                                                                                                                                                                                                              AAG-----TCAGCGGCCTGGATGAAAGAGCGGACTTCACCTGGGGCGATTCAC 1104
                                                                                                                                              LeuProTyrGluGlnAlaArgArgSerAlaTrpThrSerHisSerHisProThrGlnSer 269
                                                                               LysAlaThrGlnProSerSerThrValProLysThrGluAspGlnArgProGlnLeu 289
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297.50
34.86%
35.47%
11.50%
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Matches:
Conservative:
Mismatches:
Indels:
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	TELEPHONE: (512	٠.	
	REFERENCE/DOCKET NUMBER: LECOMMUNICATION INFORMATIO	; TE	
	NAME: Wilson Mark B. REGISTRATION NUMBER: 37,259		
	10-JAN DN: 514		
	APPLICATION DATA: ATION NUMBER: US/08/7	; ; ;	
	SYSTEM: PC-DOS/M PatentIn Release	·· ··	
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	٠. ٠.	
	ZIP: 7/210-4433 COMPUTER READABLE FORM:	 G	
	Y: USA		
	ITY: Houston		
	ADDRESSEE: ARNOLD, WHITE AND DURKEE STREET: P.O. BOX 4433	٠. ٠.	
	NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:	 G Z	
	OF INVENTION		
	CANT:		
	O. 5922688	; Patent	
	83	RESULT 15 US-08-780-	
28	72 CAGAGGGAGACAGGCTGCCCAACACCTGCCTCTGACCCCAGCATTTCCAGAGC 17	Db 16	
N	58GlyIleTyrProAsnThrArgLeuProAlaAlaHisMetProSer 47	Qy 4	
1671	21 ACCCTGGGGCAGGGGTGCTTCCTCCTCAGGCCCAGCTGCTCCCCTGGAGGA	Db 16	
457	39ValThrSerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThr	Qy 4	
1620	64GTCAGGGAGGGGCAACCAACTGCCCCAGGGGGATATGGGTCCTCTGGGGCCTTCGGG	Db 15	
438	29 PheValAlaProHisProProAlaLeuPro	Qy 4	
1563	513 TGGGGGAAAACGGGCAGTCTGCTCTGCTCTGACCTTCCAGAGCCCAAG	Db 15	
428	eAspPheHisGlyIleAlaGlnAlaLeuGlnProHisAlaHisProGl	Qy 4	
1512	.471 GGGCCTCTCCTGCCTGCCTGCCTGCCTCAGCCAG	Db 14	
408	89 LysTyrProSerAspLeuProTyrMetSerSerTyrHisGlyLysArgTyrAlaTyrLy	Qy 3	
1470	rctgagtgcctggcccagg	Db 14	
388	380ProGluSerSerMetTyr	Оу з	
1410	351 TCCATCCGCCAGTATTACAAGAAGGGCATCATCCGGAAGCCAGACATCTCCCCAGCGCCTC	pb 13	
379	367 AlaLeuArgTyrTyrAspLysAsnIleMetThrLys	Qy 3	
1350	291 GCCCGGCTGTGGGGCATCCGCAAGAACCGTCCCGCCATGAACTACGACAAGCTGAGCCGC	Db 12	
366	347 AlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArg	Оу з	
1290	CTCAGCCCAGGT	Db 12	
346	28 C	Оуз	
1230	.171 CCCATCCACCTGTGGCAGTTCCTCAAGGAGTTGCTACTCAAGCCCCACAGCTATGGCCGC	Db 11	
327	310IleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAsn	Qy	
1170	1135ACCGACAGCGAGGTGGACTCATCATGCTCCGGGCAG	Db 11	

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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281 LysThrGluAspGlnArgProGlnLeuAspProTyrGlnIle------
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 SerLysMetSerProArgValProGlnGlnAspTrpLeuSerGlnProProAlaArgVal
                                        TGATCAAACAGGAGCGCACAGACTTCGCCTACGACTCAGATGTCCCTGGATGTGCATCAA 1170
                                                                                         LysAlaLeuGlnAsnSerProArgLeuMetHisAlaArgAsnThrGlyGlyAlaThrPhe 229
                                                                                                                                                                                                                                                                        SerHisLeuHisTyrLeuArgGluThrProLeuProHisLeuThrSerAspAspValAsp 209
                                                                                                                                                                                                                                                                                                                                                                                           TyrGlyLeuProAspValAspIleLeuLeuPheGlnAsnIleAspGlyLysGluLeuCys 169
                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGCAGCCCGTGGACA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCCAGCTCTTCCCAGTCCCACCCTGGCCACGGGTACCTTGGTGAGCACAGCTCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLysHisIleProProProAsnMetThrThrAsnGluArgArgVallIeValProAla 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlyLysMetValSerSerSerAspAsnValGlyMetAsnTyrGlySerTyrMetGlu 109
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                                                                ThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSerThrValPro 280
                                                                                                                     1056
                                                                                                                                                                      IlePheProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAsp 249
                                                                                                                                                                                                                                                         -----CATCTCCTCAGGGAG----GGGGCCGGGAACCTCTCCCAGCCCCCTATCAAC
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279.50
35.22%
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	1590 TACAAGTTT 1598	րի 1
	407 TyrLysPhe 409	Qy
1589	1572	Db 1
406	Ala	Qy
1571		Db 1
386	367 AlaLeuArgTyrTyrAspLysAsnIleMetThrLysValHisProProGluSerSer	Qу
1529		Db 1
366	347 AlaArgArgTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArg	Qy
1469		Db 1
346	327 AsnCysIleThrTrpGluGlyThrAsnGlyGluPheLysMetThrAspProAspGluVal	Qy
1409		Db 1
326	307 SerGlyGlnIleGlnIeuTrpGlnPheLeuLeuGluLeuSerAspSerSerAsnSer	Qy
1349	AAGGGATTGGAGCTTTCCGGGAG-GGGCCACCCTACCAGCGC	Db 1
306	296 GlyProThrSerSerArgLeuAlaAsnProGly	Qy
1290	1231 GCTATGAAAAATCCCTTCGACCATTCCCAGATGATGTCTGCATTGTCCCTAAAAAATTTG	Db 1
295	295	Qy
1230	1171 TGTACCTCCACCCAGAGGGCTTCTCTGGACCCTCTCCAGGTGATGGAGTGATGGGTTATG 1230	Db 1

Search completed: November 9, 2002, 19:49:16 Job time: 75.0549 secs

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Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09902772/runat_07112002_134035_9131/app_query.fasta_1.1294
-DB=Published_Applications_NA -QEMT=fastap -SUPETX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000000 -USER=US0902772_@CGN 1_1_46_@runat_07112002_134035_9131
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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2588
1 MASTIKEALSVVSEDQSLFE...
                       Query
                                                                                                                is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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    Match
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Sequence Sequence Sequence

18410, A 20472, A 54, Appl 3705, Ap

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MICROARRAY		sequence 1, Appl. sequence 1716, Ap sequence 1693, Ap sequence 1693, Ap sequence 29364, A sequence 29364, A sequence 1798, Ap sequence 1747, Ap sequence 1748, Ap sequence 178, Ap sequence 237, Appl sequence 237, Appl sequence 11, Appl sequence 11, Appl sequence 10, Ap sequence 44, Appl sequence 1680, Ap sequence 1680, Ap sequence 1680, Ap sequence 1680, Ap	equence 1653, A

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OR APPLICATION NUMBER: PCT/US01/00661
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OR APPLICATION NUMBER: PCT/US01/00670
IOR APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00662
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IN HELLO, SIGNAL = 1.4
IN HELA, SIGNAL = 1.7
IN HEART, SIGNAL = 0.92
IN BONE MARROW, SIGNAL = 2.1
IN LUNG, SIGNAL = 1.8
IN BRAIN, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.5
IN ADULT LIVER, SIGNAL = 1.5
IN BT474, SIGNAL = 1
IN BT474, SIGNAL = 0.95
HIT: P11308, EVALUE 9.00e-99
HIT: P11308, EVALUE 0.00e+00
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PRIOR FILLING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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Sequence 54, Application US/09923779
Patent No. US20020076721A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
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; LOCATION: 356, 363, 417,
; LOCATION: 537, 545
; OTHER INFORMATION: n = A,
US-09-923-779-54
                                                                                                                       US-09-864-761-3705/c
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DB:
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Best Local Similarity:
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 549
                                                                                  Sequence 3705, Application Patent No. US20020048763A1 GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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FILING DATE:

APPLICATION NUMBER: US 60/180,312

2000-02-04

APPLICATION NUMBER: US/09/864,761 FILING DATE: 2001-05-23

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R APPLICATION NUMBER: PCT/USO1/00668
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/USO1/00663
R APPLICATION NUMBER: PCT/USO1/00663
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ER INFORMATION: EXPRESSED I
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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IN ADULT LIVER, SIGNAL =
IN FETAL LIVER, SIGNAL =
IN BRAIN, SIGNAL = 1.1
IN BOAL MARROW, SIGNAL = 0.
IN PLACENTA, SIGNAL = 1.5
IN HBLLOO, SIGNAL = 1.4
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US-09-864-761-1653/c; Sequence 1653, Application; Patent No. US20020048763A1
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                 NUMBER
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OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: US
FILING DATE: 2000-09-27
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Chen, Wensheng
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                  NOS: 49117
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OTHER INFORMATION: MAP TO APOOR
OTHER INFORMATION: EXPRESSED IN
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fyddoro, Dmitry V.
TITLE OF INVENTION: Reagents and Methods for the Screening TILLE OF INVENTION: Useful in the Treatment of Neurological Title OF INVENTION: USEful in the Treatment of Neurological Title OF INVENTION: USMBER: US/09/850,799
CURRENT APPLICATION NUMBER: US/09/850,799
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 454
TYPE: DNA
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ED IN HELA, SIGNAL = 1.7
ED IN HEART, SIGNAL = 0.92
ED IN BONE MARROW, SIGNAL = 2.
ED IN LUNG, SIGNAL = 1.8
ED IN BRAIN, SIGNAL = 1.5
ED IN ADULT LIVER, SIGNAL = 1.
ED IN BT474, SIGNAL = 1.
ED IN FETAL LIVER, SIGNAL = 0.
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rSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerPro
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                 AGCCGCCGCCCAGGATGGCGCACTTTACAAGCTCCCGGCTGGTCTGGCTCCACTGCCCTT
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967	908 GAGCAGGAGTTTCAGATGTTCCCCAAGTCTCGGCTCAGCTCAGCGTCACCTACTG
218	Ov 208  AspLysAlaLeuGlnAsnSerProArgLeu
907	848 CCCAAAGGCGGCCTCCTGGACAGCATGTGTCCGGCCTCCACACCCAGCGTACTCAGCTCT
208	Qy 199ProLeu-ProHisLeuThrSerAspAspVa
847	Db 788 AGCAATACATTAGGTTTTGGCACAGAGCAGGCGCCCTATGGAATGCAGACACAGAATTAC
198	Qy 197 GluThr
787	Db 728 AAGACAGAAGATCAATATGAAGAAAATTCACACCTCACCTCCGTTCCTCATTGGATTAAC
196	
192 727	Qy 182 SerTyrAsnAlaAspIleLeuLeuSerHisLeu
667	::::::   :::     :::
181	162
161	Qy 142 TrpLeuGluTrpAlaValLysGluTyrGlyLeuProAspValAspIleLeuLeuPheGln
550	Db 491 CAGCGCCCTGGCCATTCCAAAGAACCCCTGGCTGTGGAGCAACAGGTATGCCAG
141	Oy 122 GluargargValIleValProAlaAspProThrLeuTrpSerThrAspHisValArgGln
	US-09-902-772-4 (1-478) x US-09-920-300A-1716 (1-2188)
	Alignment Scores: 1.82e-34 Length: 2188  Score: 444.00 Matchbas: 138  Percent Similarity: 38.36% Conservative: 45  Best Local Similarity: 28.93% Mismatches: 134  Query Match: 17.16% Indels: 161  DB: 10 Gaps: 16
	920-300A-1716
	CORRENT CORRENT CORRENT NUMBER SOFTWAN SEQ ID N LENGTH TYPE: ORGANI
	APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOSITIONS AND MITTLE OF INVENTION: AND DIAGNOSIS OF FILE REFERENCE: 210121.547
	-09-920- Sequence Patent N GENERAL APPLICA APPLICA
	SULT 7
	Qy 467 -AlaAlaHisMetProSerHisLeuGlyThrTyrTyr 478 
466 1091	Qy 456ThrGlyGlyIleTyrProAsnThrArgLeuPro
1031	Db 996 CTCTTACTGGCCTGGTCCCAACGCCACCGCCGCTGC

ULT 8 10-033-528-1716 equence 1716, Application US/10033528 atent No. US20020131971A1 EMERAL INFORMATION: BAPPLICANT: King, Gordon E. APPLICANT: Weagher, Madeleine Joy APPLICANT: Xu, Jiangchun	RESULT 8 US-10-033-528 ; Sequence 171 ; Patent No. U ; Patent No. I ; PATENT INFO ; APPLICANT: ; APPLICANT: ; APPLICANT:
1 oAsnThrargLeuProAlaalaHisMetProSerHis 473	Qy 46 Db 176
GAAAGGCAGGATTGAAAATGTC	Db 17
2	
6 aLeuProValThrSerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProTh 45	
- GCCGTCCAGCCCGACACGGAGGACTGAGGTCGCCGGGACCAC	Db 159
6 nAlaLeuGlnProHisAlaHisProGlnLysMetAsnPheValAla	0у 41
7 CGTGTGCGACCTCCAGAACTTGCTGGGGTTCACGCCCGAGGAACTGCACGCCATCCTG 1594	Db 1537
- (D	Qy 409
1TCGGGAAGCGCTACGTGTACCGCTT 1536	Db 1511
9 sTyrProSerAspLeuProTyrMetS	0у 38
7 CTACTATTACGACAAGAACATCATCCACAAGACG 1510	Db 147
9 9	Ωу 36
9 gTrpGlyGluArgLysSerLysProAsnMetAsnTyrAspLysLeuSerArgAlaLeuAr 369	Qy 34 Db 141
	Db 135
9	Qу 32
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09 nIleGlnLeuTrpGlnPheLeuLeuGluLeuLeuSerAspSerSerAsnSerAsnCysIl 329	Qy 3
9 uAspProTyrGlnIleLeuGlyProThrSerSerArgLeuAlaAsnProGlySerGlyGl 309 ::             8 ACCTGCAGCTGTGCTGGCCGGCTTCACA	Qy 28 рь 125
05 AAGGATTACATCCAAGAGAGGAGTGACCCAGTG-GAGCAAGGCAAACCAGTTAT 1257	Db 12
9 rLysAlaThrGlnProSerSerSerThrValProLysThrGluAspGlnArgPr	Qу 26
5 GAGAGCTTCGAAGATGACTGCAGCCAGTCTCTCTGCCTCAATAAGCCAACCATGTCTTTC 1204	Db 1145
61ThrSerHisSerHisProThrGlnSe 269	Ωу 2
 CTCCTCCAGTCCTGGAACA	Db 1085
51 oTyrGluGlnAlaArgArgSerAlaTrp 260	Оу 2
8 CCCAAAGACCACGACTCCCCTGAGAACGGTGCGGACAGCTTCGAGAGCTCAGACTC	Db 102
31 eProAsnThrSerValTyrProGluAlaThrGlnArgIleThrThrArgProAspLeuPr 251	0у 2
:::       ::         ::	Db 96
219 -MetHisAlaArgAsnThrGlyGlyAlaThrPheIlePh 231	Qy 2

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; APPLICANT: Secrist, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
: FILE REFERENCE: 210121.547C1
: CURRENT APPLICATION NUMBER: US/10/033,528
: CURRENT FILING DATE: 2001-12-26
: NUMBER OF SEQ ID NOS: 1896
: NOTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1716
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1716
: LENGTH: 2188
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-033-528-1716
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{\tt rLysAlaThrGlnProSerSerSerThrValProLysThrGluAspGlnArgProGlnLe}
                                  GAGAGCTTCGAAGATGACTGCCAGCCAGTCTCTCTGCCTCAATAAGCCAACCATGTCTTTC
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h: 2268 les: 138	ENT FILING DATE: 2001-07-31  ERR OF SEQ ID NOS: 1789  WARE: FastSEQ for Windows Version 4.0  D NO 1693  GTH: 2268  E: DNA  ANISM: Homo sapiens 20-300A-1693  nt Scores: 1,92e-34  Match  Similarity: 38.36% Conse	SE SE SE SE SE SE SE SE SE SE SE SE SE S
0A  METHODS FOR THE THERAPY F COLON CANCER 0,300A	20-300A-1693 20-300A-1693 nce 1693, Application US/0992030 ft No. US20020136728A1 AL INFORMATION: ICANT: King, Gordon E. ICANT: Meagher, Madeleine Joy ICANT: Weagher, Madeleine Joy ICANT: Secrist, Heather ICANT: Secrist, H	US-09-01 Sequent Patent Patent Patent Patent Patent Patent Patent Papel
AACGGCAC 18	65 CAAACCACGCCTCTT	
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CAAGAAGCAGTGGCCTTATTCCATCC	456 rGlyGly	p 2
ProAsnProTyrTrpAsnSerProTh    :::  CTGACCAGCTGCTCCGAGGACCCAG	436 aLeuProValThrSerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerPro	Qy Db 1
roGlnLysMetAsnPheValAlaProHisProProAl        ACTGAGGTCGCCGGGACCACCCTGAGCC	416 nAlaLeuGlnProHisAlaHisProGlnLysMetAsn :::       1595 -GGCGTCCAGCCCGACACGGAGGACTGAGGTCGCCGG	Qу рь 1
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Db 631 TGCTTCTTGGGCCACCAATGAGTTCAGTCTGGTGAACGTTGCAGAGGTTC  Oy 162 AsnileAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThrPro	US-09-902-772-4 (1-478) x US-10-033-528-1693 (1-2268)  QY 122 GluArgArgValIleValProAlaAspProThrLeuTrpSerThrAspHisValArgGln :::	Alignment Scores: 1.92e-34 Length: 2268 Pred. No.: 444.00 Matches: 138 Percent Similarity: 38.36% Conservative: 45 Best Local Similarity: 28.93% Mismatches: 134 Ouery Match: 17.16% Indels: 161 DB: 12 Gaps: 16	Qy 369 gTyrTyrTyrAspLyaAsilleMeThiLysValHisProProGluSerSerMetTyrLy Db 1557 CTACTATTACGACAAGAACATCATCCACAAGACG	
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OTHER INFORMATION: MAP TO APO01426.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN BRAIM, SIGNAL = 0.45
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
OTHER INFORMATION: SWISSPROT HIT: P11308, EVALUE 4.00e-38
OTHER INFORMATION: MT HIT: M21535.1, EVALUE 1.00e-113
OTHER INFORMATION: EST_HUMAN HIT: AW948986.1, EVALUE 1.00e
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LENGTH: 348
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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R FILING DATE: 2001-01-30

DR APPLICATION NUMBER: PCT/US01/00664

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00669

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: US 09/600,...
APPLICATION NUMBER: US 09/774,203
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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CURRENT FILING DATE: 2001-05-23
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OR APPLICATION NUMBER: PCT/USO1/00669

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OR APPLICATION NUMBER: PCT/USO1/00665

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00668

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00663

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/USO1/00662

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                                 OR APPLICATION NUMBER: PCT/US01/00670
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
OR APPLICATION NUMBER: US 09/608,408
OR FILING DATE: 2000-06-30
OR APPLICATION NUMBER: US 09/774,203
OR FILING DATE: 2001-01-29
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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; OTHER INFORMATION:
US-09-864-761-5035
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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LENGTH: 477
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                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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APPLICANT: Rank, David F
APPLICANT: Hanzel, David
APPLICANT: Chen, Wensher
                                                                      PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT. PRIOR FILING DATE: 2001-01-30
                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo
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                               APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                             APPLICATION NUMBER: PCT/US01/00669
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Hanzel, David K.
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                      LeuSerHisLeuHisTyrLeuArgGluThrProLeuPro 201
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US-09-864-761-7427/c
; Sequence 7427, Application
; Patent No. US20020048763A1
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Query Match:
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2011-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine SEQ ID NO 12798
LENGTH: 519
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Abounica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
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APPLICANT: Penn, Sharron G.
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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IN ADULT LIVER, SIGNAL =
IN BRAIN, SIGNAL = 0.45
IN FETAL LIVER, SIGNAL =
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SOUTWARE: Annomax Sequence
SEQ ID NO 7427
LENGTH: 553
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       Percent Similarity:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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R APPLICATION N
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00667
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ACCATCAAAATGGAATGTAACCCTAGCCAGGTGAATGGCTCAAGG
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ESSED IN PLACENTA, SIGNAL = 2.1
ESSED IN BONE MARROW, SIGNAL = 2.
ESSED IN LUNG, SIGNAL = 1.3
ESSED IN ADULT LIVER, SIGNAL = 0.
ESSED IN HEART, SIGNAL = 2.1
ESSED IN FETAL LIVER, SIGNAL = 2.
ESSED IN BRAIN, SIGNAL = 2.
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Search completed: November 9, 2002, 21:28:47 Job time: 78.9473 secs

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-MODEL-frame+_pln.model -DEV=xlp
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-(-Cgn2_1/USPT0_Spool_VG9902772/runat_07112002_134034_9041/app_query.fasta_1.1294
-0-/cgn2_1/USPT0_Spool_VG9902772/runat_07112002_134034_9041/app_query.fasta_1.1294
-DB=EST -OPMT-fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MILEN-0 -MAXLEN-2000000000
-USER-US09902772_eCGN_1_1_2221_erunat_07112002_134034_9041 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BM456833	RESULT 1
1 (bases 1 to 1045) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BM456833.1 GI:18505873	BM456833	5', mRNA sequence.	AGENCOURT_6404041 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583753	BM456833 1045 bp mRNA linear EST 05-FEB-2002		

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                                                        TyrMetGluGluLysHisIleProProProAsnMetThrThrAsnGluArgArgVallle
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GAACTGTGCAAGATGACCAAGGACGACTTCCAGAGGCTCACCCCCAGCTACAACGCCGAC
                            GluLeuCysLysMetThrLysAspAspPheGlnArgLeuThrProSerTyrAsnAlaAsp 186
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http://image.llnl.gov
plate: LLAMI2347 row: f column: 10
High quality sequence stop: 669.
Location/Qualifiers
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Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/fissue_type="embryonal carcinoma, cell line"
/fissue_type="embryonal carcinoma, cell line"
/flab_host="DHIOB (phage=resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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5', mRNA sequence.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae;
1 (bases 1 to 880)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN13279 row: h column: 07
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Contact: Robert St
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/clone="IMAGE:6041526"
/clone_lib="NIH_MGC_92"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                            BM489636 634 bp mRNA linear EST 07-FEB-200 pgm2n.pk011.124 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk011.124 5' similar to spl(990837) ERG_CHICK TRANSCRIPTIONAL REGULATOR ERG pir|S60754 transcription factor erg chicken emb|CAA54404.1| (X77159) ERG [Gallus gallus], mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
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Eukaryota; Metazoa;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pow/SPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal grow plate 33.3% of the final RNA pool). Single pass sequenci from 5'-end"

164 c 138 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
/strain="Commercial broiler
strains 90 & 21"
/db_xref="taxon:9031"
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/clone_lib="Normalized Chicl
and Epiphyseal Growth Plate
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/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male and Female"
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AĞENCOURT_7571287 NIH_MGC_92
5', mRNA sequence.
BQ212127
BQ212127.1 GI:20392058
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM13307 row: b column:
High quality sequence stop: 562.
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                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 1089)
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Location/Qualifiers
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                                                                                                              /tissue_type="embryonal carcinoma, cell line"
/lab_host="pH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 314 c 257 g 225 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:6052136"
/clone_lib="NIH_MGC_92"
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AACGAGCGCAGAGTTATCGTGCCAGCAAGATCCTACGCTATGGAGTACAGACCATGTGCG
                                                                         GlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProProAsnMetThrThr
                                                                                                                                 SerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnVal
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            AsnGluArgArgValI1eValProAla-AspProThrLeuTrpSerThrAspHisValAr 140
                                                         GGGATGAACTACGGCAGCTACATGGAGGAGAAGCACATGCCACC-CCAAACATGACCACG
                                                                                                                     TCTCCTGATGAATGCAGTGTGGCCAAAGGCGGGAAGATGGTGGGCAGCCCAGACACCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10429 row: m column: 13
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
Unpublished (1999)
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Clone distribution: MGC clone distribution information
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(bases 1 to 915)
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   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryonal carcinoma, cell line"
/lab_host="hH10B (phage_resistant)"
/note="Organ: testis; Vector: pcNV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
a 252 c 227 g 190 t
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/clone_lib="NIH_MGC_92"
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/db_xref="taxon:9606"
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1 (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ; testis; Vector: pCMV-SPORT6; Si:
Site_2: Sall; Cloned unidirectionally; oligo-
                                                                                 /clone="IMAGE:4521233"
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Simpson A.J.G.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Brazil
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National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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/clone="IMAGE:4509541"
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Yamamoto, J.,
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Genomics Laboratory
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/tissue_type="placenta"
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Email: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information
Washington University Genome Sequencing Center For information
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Other_ESTs: 1e01d08.xl
Contact: Douglas Melton, Klaus H. Kaestner
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theislang,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y., and Bowers,Y.
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h quality sequence stop:
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/db_xref="taxon:9606"
/clone="IMAGE:5085758"
/clone_lib="HR85 islet"
/tissue_type="Purified par
/lab_host="DH108"
                                                                                                                                                                                                     /note-*Organ: Pancreas; Vector: pBluescript SK(-); Site_1: Not1; Site_2: Xho1; cDNA made by oligo-dT priming.

Size-selected on agarose gel. Average insert size -1kb. 5'
Xho1 site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692.*
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                                           Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tayawai, M., Tayawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
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Arakawa, T., Carninci, P., Fukuda, S.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                   BB660034
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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CDNA clone D430027L04 5', mRNA sequence
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                                                                                  TGTGCCTACGGAACGCCACACCTGGCTAAGACAGAGATGACCGCATCCTCTCCAGTGAC
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su,Y. and Hayashizaki,Y.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Hayashizaki,Y.
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further details.
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Project of Genome Exploration Research Group in Riken
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/db_xref="taxon:10090"
/clone="D430027L04"
/clone_lib="RIKEN full-length
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/dev_stage="13 days embryo"
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                                                                                  PCR PRIMER'S
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGACG
BACKWARD: D COLUMN: 21
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                    Keele, J.W.

Sequence evaluation of four pooled-tissue normalized Libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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501436 MARC 2BOV Bos taurus
BM088063
BM088063.1 GI:16998691
EST.
                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
vd. 980904.e. Vector identified by crc
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                       Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_11b="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                       Location/Qualifiers
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                                         Gallus gallus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                         Buerstedde, J.M.
                                 (bases 1 to 827)
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Library made from pooled tissue from testis, thymu semitendonosus muscle, longissimus muscle, pancrea adrenal, and endometrium."

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AsnMetAsnTyrAspLysLeuSerArgAlaLeuArgTyrTyrTyrAspLysAsnIleMet
                          SerAlaTrpThrSerHisSerHisProThrGlnSerLysAlaThrGlnProSerSerSer
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html
Location/Qualifiers
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/dev_stage="2-3 weeks old"
/note="CB inbred strain"
236 c 177 g 181 t
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/db_xref="taxon:9031"
/clone="8m13r2"
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	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	RESULT 14 BB639043 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 458 of the April 19	Qy 438 Db 761	Qy 421 Db 701	Qy 418 : Db 641	Qy 398 Db 590	Db 581	521 378
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura,S., Kawaai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Ronno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a	., Miyazaki,A., Nomura,K., Ohno,M., to,R., Sakai,C., Sakai,K., Sano,H., a,A., Shiraki,T., Sogabe,Y., Suzuki ahashi,F., Takeda,Y., Tanaka,T., To aki,Y., to, et al. 2001) izaki loration Research Group, RIKEN Gencohama Institute	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 675) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Tahii,Y., Ito,M., Kawai,T., Kongo, H., Kawai, T., Kongo, H., Kongo, H., Kongo, H., Kongo, H., Kongo, H., Kawai, T., Kongo, H., Kongo, H., Kawai, T., Kongo, H., Kongo, H., Kawai, T., Kawa	BB639043 BB639043 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630068021 5', mRNA sequence. BB639043 BB639043.1 GI:15401323 EST. house mouse.	GlyIle 459     AGCATT 826	ProValThrSerSerSerPhePheAlaAlaProAsnProTyrTrpAsnSerProThrGly 457 	HisAlaHisProGlnLysMetAsnPheValAlaProHisProProAlaLeu 437	LeuGlnPro 420                    CTCCAGCCTCATCCCACTGAATCATCAATGTACAAGTATCCATCAGATCTCTCCTACATG 700	SerSerTyrHisGlyLysArgTyrAlaTyrLysPheAspPheHisGlyIleAlaGlnAla 417 	ThruysvalhisproproglusersermetryrlystyrproseraspleuproTyrmet 397	

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Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                       sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Shibata, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koud, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasak, D., Shibatta, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., I',
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
varantizaki,V., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group,
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Human Genome Sequences
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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of Full-Length Mouse cDNAs Mamm. Genome. 12, 673-677 (2
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    As Compared with (2001)
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AsnGluArgArgVallleValProAlaAspProThrLeuTrpSerThrAspHisValArg
                                            GlyMetAsnTyrGlySerTyrMetGluGluLysHisIleProProProAsnMetThrThr
                                                                                                                     SerProAspAspCysSerValAlaLysGlyGlyLysMetValSerSerSerAspAsnVal
                                                                                                                                                                                 ProAlaArgValThrIleLysMetGluCysAsnProAsnGlnValAsnGlySerArgAsn
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                                                                                                      TCACCTGATGAGTGCAGTGTGAACAAAGGTGGGAAGATGGTGGGCAGCCCGGATACTGTG
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Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Lambda FLC I.
BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/GJ"
/db_xref="faxon:10090"
/clone="6330501C04"
/clone_1ib="RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="yH10B"
/note="Site_1: SalI; Site_2: Bami
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                  ProSerTyrAsnAlaAspIleLeuLeu 189
                                                                                                                                                                                       AATGAGCGCAGAGTGATCGTCCCTGCAGATCCTACTCTGTGGAGCACAAGACCATGTCCGA 480
                                                                             GlnasnIleAspGlyLysGluLeuCysLysMetThrLysAspAspPheGlnArgLeuThr
                                                              CAGAATATCGATGGGAAGGAGCAGTGCAAGATGACATANGATGACTTCCAGCGGCTCACG
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Copyright (c) 1993 - 2002 Compugen Ltd
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AF218944/c LOCUS DEFINITION ACCESSION VERSION		C 44 45	4 4 3 2			c 3/				c 31				25	24	22		c 19		c 16	14	12	11		c 8 ^	100	с (л. #		ი ი 2 I	1 2 0	
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DNA stage;	linear VRL 18-JUL-2000 RNA polymerase gene,		ence ence	44 5 E	547 Sequence I	1 Sequenc	A40968 Sequence 37	A97517 Sequence 17	AX404317 Sequence	AR209935 Sequence	AR107992 Sequence AR144253 Sequence	AR095805 Sequence	X56223 M.vison B-2	AX204206 Sequence	מ ע	AR011922 Sequence AR017793 Sequence	AR084537 Sequence	AR079236 Sequence AR118353 Sequence	O t	AX154058 Sequence A86933 Sequence 24	メセ	L10902 Mus musculu	י עם מ	שם	ດນ	M94403 Artificial G31952 MCW92 Chick	æ	AX453551 Sequence 2	793 Mus	AF218944 Norwalk v C75748 Homo sapien	cription	

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         Mus musculus APC2 gene,
AJ130793
AJ130793.1 GI:4210442
APC2 gene.
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Asakawa,S. and Shimizu,N.
Asakawa,S. and Shimizu,N.
Direct Submission
Submitted (09-SEP-1997) Shuichi Asakawa, Keio University School
Medicine, Department of Molecular Biology; Shinanomachi 35,
Shinjuku-ku, Tokyo 160, Japan (E-mail:asa@dmb.med.keio.ac.jp,
Tel:81-3-3351-2370)
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C75748
C75748.1 GI:3176190
STS; DH; Digital hybridization.
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                                                                                                                                                                                                                                                                                                                                                      Asakawa, S. and Shimizu, N.
High-fidelity digital hybridization
Genomics 49 (2), 209-217 (1998)
98260670
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                                                      MMU130793
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/strain="Hu/NV/SN85JA-1/85/JP"
/db_xref="taxon:11983"
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2 (bases 1 to 78)
van Es,J.H., Kirkpatrick,C., van de Wetering,M., Molenaar, Miles,A., Kuipers,J., Destree,O., Peifer,M. and Clevers,H. Identification of APC2, a homologue of the adenomatous polynomials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-NOV-1998) van Es J.H., Hospital Utrecht, Heidelberglaan 101 NETHERLANDS
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Curr. Biol. 9 (2), 105-108 (1999)
99147086
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                                                                                                                                                                                                                electrophoresis
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                                                                                                                                                                                                                                                                                       Unknown
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Eukaryota; Metazoa;
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1 (bases 1 to 78)
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/product="APC2 |
/number=11
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/db_xref="taxon:10090"
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triplex-affinity
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                                       SYNPRWA 47 bp DNA Artificial gene pRW2701 synthetic fragment M94403
                                                                                                                                                                                                                                                                   (NO)
                                                                                                                                                                                                                                                                          Patent: WO 0244215-A 38 06-JUN-2002;
REKKE OLE HENRIK ANDRE (NO); SANDLIE INGER (NO); LAUVRAK VIGDIS
                                                                                                                                                                                                                                                                                                                                       synthetic construct. synthetic construct
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REKKE OLE HENRIK ANDRE (NO); SANDLIE INGER (NO); LAUVRAK VIGDIS
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Reservota; Metazoa; C
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Box 338, 6700 AH Wageningen, The Netherlands
Email: richard.crooijmans@alg.vf.wau.nl
Primer A: GATCCTCATGABTACAGGTT
Primer B: GATCGCAABACGCCTTTGTG
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                                                                                                                                                                                                                                                                                                    Contact: Richard Crooijmans
Department of Animal Breeding
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New microsatellite markers in chicken
fluorescent genotyping
Anim. Genet. 28 (6), 427-437 (1997)
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1 (bases 1 to 72)
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G31952.1 GI:2137898
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MCW92 Chicken RPMACrooijmans Gallus
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                                                                                    Annealing:
Polymerization:
PCR Cycles:
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92381066
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/db_xref="taxon:32630"
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/db_xref="taxon:9031"
/clone_lib="Chicken RPMACrooijmans"
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                                                                                                            27-APR-1993
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extrusion

facilitates

intramolecular

triplex

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RESULT 14
MUSCEREBI
LOCUS
DEFINITION
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AUTHORS
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AUTHORS
          ACCESSION
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effects
J. Biol.
92381066
1512273
                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-JUN-2001) Department of Molecular and Cellular
Biology, Medical Institute of Bioregulation, Kyushu University,
3-1-1, Maidashi, Higashi-ku, Fukuoka-shi 812-8582, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F391178S02 94 bg
Mus musculus F-box-WD40 repeat
AF391179
                                                                                                                                                                                                                                                                                                                                                                            and Nakayama, K.I.
Characterization of a Mouse Gene of Caenorhabditis elegans SEL-10
                     L10902
                               Mus musculus (clone
          L10902.1
                                                                                                                                                                                                                                                                                                                                                                    Genomics 78 (3), 214-222 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                          MUSCEREBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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                                                                                                                                         Conservative
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                                                                                                                                                                                            /gene="Fbxw1"
/number=2
a 18 c
                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="129/Sv"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
13 c 27 g 24 t
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93.38;
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93.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                              99 bp
Gcap15) mRNA
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                                                                                                                                      Score 13.4; DB 10;
Pred. No. 1.2e+04;
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Pred. No. 1.2e+04;
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                                                                                                                                                                                             19
                              sequence
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                                         mRNA
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TITLE
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MEDLINE
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BASE COUNT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 66)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L. selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                           Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA
                                                                                                                                                                                                                                                                           2 (bases 1 to 66)
Striebich,C.C., Falta,M.T., Wang,Y.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TCRB) mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel cDNA clones obtained cerebellar cDNA expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 99)
Kambouris, M. Ph.D., Sangameswaran, L.,
Dlouhy, S.R., Ghetti, B. and Hodes, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF043830.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1993)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (library: lambda ZAP) neonate cerebellum Mus musculus
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/note="Contains the
end of the TCRBJ."
/codon_start=1
                                                                                                             /tissue_type="peripheral blood"
/note="from rheumatoid arthritis patient CS-2 [TCRBV17]
[TCRBJ1S5]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="neonate"
/tissue_lib="lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/haplotype="Pl_wv/+"
                                                /gene="TCRB"
                                                                             /gene="TCRB"
                                                                                                                                                             /clone="34"
                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="cerebellum"
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                                                                                                                                                                                                                . .66
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93.3%;
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Rodentia;
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Pred. No. 1.2e+04;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 bp
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library
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                                 end
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1 T cell
                                 of TCRBV, the nDn,
                                                                                                                                                                                                                                                                                          В111, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triarhou, L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
receptor
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beta
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chain CDR3
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Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                              No.
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1: /SIDS2/gcgdata/g
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3: /SIDS2/gcgdata/g
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Copyright (c) 1993 - 2002 Compuc
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ABN02626	9	AAX81695		AAV59955	53		o	AAQ34153	ന	ABN54420	AAA77247	AAI68326	ABS14344	AAI06802	AAI46343	AAI21082	AAK40324	AAK14578	32	ABA66159	ABA48277	ABN58012	AAC15545	AAC15530	ABN40404	AAQ78847	ABQ75848	ABQ75846	368	N	962	556	556	556	ABN05561
LP-1 17	DNA contain	Primer used in a n	Oligonucleotide id	11-	Sis F	elic m	Human SCYA24 ASO p	Downstream sequenc	~	spliced tra	n clone	related PCR	genome-deri	#6793 L	#15029 used	#1101	bone marrow	brain e	#11694	foetal	breast c	spliced t		secreted	n spliced	v Ab lig	primer	primer FCRIFC	ex	6 polymo	SR-cyp anti	GDMLP-1 25-	GDMLP-1 25-	GDMLP-1 2	Human GDMLP-1 25-m

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## ALIGNMENTS

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RESULT 1
ABN30396
Shoshan A,
                                                                         28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                       Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
                       WPI; 2002-257383/30.
                                                                                                                      07-FEB-2002
                                                                                                                                      WO200210449-A2
                                                                                                                                                                                                Rat spliced transcript detection oligonucleotide SEQ ID NO:3144.
                                                                                                                                                                                                                                    ABN30396;
                                                                                                                                                                                                                                                     ABN30396 standard; DNA; 65 BP
                                                        (COMP-) COMPUGEN INC
                                                                                                   20-JUL-2001; 2001WO-IB01903
                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                   15-JUL-2002
                                        Wasserman
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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription

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N.B. The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from MIPO and the property of the printed as the property of the printed as pecification, but was obtained in electronic format directly from MIPO and the property of the printed as the property of the printed as pecification, but was obtained in electronic format directly from MIPO and the property of the printed as the property of the printed as pecification, but was obtained in electronic format directly from MIPO and the property of the printed as the property of the printed and the property of the property of the printed and the property of the property 
New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription
                                                                           WPI; 2002-257383/30.
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02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
                                                                                                                                                                         (COMP-) COMPUGEN INC
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                                                                                                                                                                                                                                                                                                                                                   07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65
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at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse;
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                                                                                                                      Wasserman
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                                                                                                                                                                                                                       2000US-221607P
2001US-287724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat; splice transcript; detection; RNA transcript;
t; transcriptome; oligonucleotide library; ss.
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94.1%;
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ABN45059/c ID ABN45059 standard; DNA; 60
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Cc several oligonucleotides, each capable of hybridising selectively to a
Cc set of messenger RNAs transcribed from a given transcription unit of
Cc the genome, which encodes one or more messenger RNA splice variants.
Cc The oligonucleotide libraries are useful for detecting mRNAs from a
Cc biological sample, in expression profilling studies, in qualitatively or
Cc quantitatively characterising the corresponding transcriptome, and in
Cc detecting RNA transcripts and splice variants of human or animal
Cc transcriptomes. The libraries may also be used as specialised mini
Cc libraries to detect transcripts of a sub-transcriptome under a
Cc particular biological or pathology-specific genes such as those genes
Cc only expressed in specific tissue under a specific pathological
Cc condition; to detect developmental specific genes such as those genes
Cc only expressed in specific tissue under a specific pathological
Cc condition; to detect developmental specific genes; and to detect RNA
Cc transcripts and splice variants of a transcriptome of a patient suffering
Cc from a particular disorder. ABN27253 to ABN9589 represent
Cc oligonucleotide sequences from rats, humans and mice, which are used in
Cc N.B. The sequence data for this patent did not form part of the printed
Cc specification, but was obtained in electronic format directly from WIPO
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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription
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02-MAY-2001; 2001US-287724P
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                                                                      WPI; 2002-257383/30.
                                                                                                                 Shoshan A, Wasserman
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t; transcriptome; oligonucleotide library;
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Best Local (
26-MAY-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a
                                                                                                                                                                                             06-DEC-2001.
                                                                                                                                                                                                                           WO200192524-A2
                                                                                                                                                                                                                                                                                                  muscle;
                                                                                                                                                                                                                                                                                                               Human; genome-derived myosin-like protein 1; GDMLP-1;
                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN02627 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                several oligonucleotides, each capable of hybridising selectively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             messenger RNAs that populate a (sub-)transcriptome, where (sub-)transcriptome comprises messenger RNAs transcribed f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome, useful for detecting tissue-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                  myosin;
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2000US-207456P.
2000US-234687P.
2000US-236359P.
2000GB-0024263.
2001WO-US00661.
2001WO-US00663.
2001WO-US00664.
2001WO-US00664.
2001WO-US00666.
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                                                                                                                                                                                                                                                                                   disorder;
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Pred. No.
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                                                                                                                                                                                                                                                                                                 therapy;
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2.5e+03;
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RESULT 5 ABN05556

ABN05556 standard; DNA;

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muscle; myosin;
skeletal muscle

Human; genome-derived myosin-like protein 1; GDMLP-1;

chromosome 22; gene
disorder; amplicon;

therapy; vaccine; screening; ss.

heart disease;

Human GDMLP-1 25-mer scanning

SEQ

ID

NO:4 sequence

SEQ

ID NO:5548

29-MAY-2002 (first entry)

WO200192524-A2

Homo sapiens

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                                                                     Matches
                                                                                                     Query Match
                                                                                                                                                                                                                               of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynuclectide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering
                                                                                                                                        Sequence
                                                                                                                                                                                     N.B. The sequence data for this patent did not specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide, for raising antibodies that recognize hGDMLP-l proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human
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                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                                                                                                        invention.
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l Similarity
15; Conserv
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2001WO-US00668.
2001WO-US00669.
2001WO-US00670.
2001US-266860P.
                                                                     Conservative
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                                                                                                                                    5 C;
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88.2%;
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The protein
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                                                                                   Score 13.8;
Pred. No. 2
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RESULT 6
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controlled initial substrates for the recombinant engineering
cof hGDMLP-1 protein variants having desired phenotypic improvements, and
core expressing the proteins. The hGDMLP-1 proteins or polypeptides may
be used as immunogens to raise antibodies that specifically recognise
concentration and/or amount specifically of hGDMLP proteins, as specific
concentration and/or amount specifically of hGDMLP proteins, as specific
concentration, as therapeutic supplement in patients having specific
deficiency in hGDMLP-1 production, and in vaccines or for replacement
therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
concentration and skeletal muscle disorders. hGDMLP-1 is localised to
concentration and skeletal muscle disorders. hGDMLP-1 is localised to
concentration of the present sequence represents an oligome used in the
                                                                                                                                                                    Query Match
Best Local S
Matches 15
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21-SEP-2000;
27-SEP-2000;
              ABN05557;
                                         ABN05557 standard;
                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                screening of the hGDMLP-1 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide, for raising antibodies that proteins, or as specific biomolecule capture psurface-enhanced laser desorption ionization, myosin-like protein hGDMLP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ
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30-JAN-2001;
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2001WO-US00661
2001WO-US00663
2001WO-US00663
2001WO-US00665
2001WO-US00665
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2001WO-US00666
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                                         DNA;
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88.2%;
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30-JAN-2001;
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21-SEP-2000;
27-SEP-2000;
                                                                              of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present
Sequence
                                                                                                                                                                                                                                                              hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and
                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide, for raising antibodies that proteins, or as specific biomolecule capture proteins or a specific biomolecule capture proteins description ionization, myosin-like protein hgDMLP-1
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                                          N.B. The sequence data for this patent did not specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                    The present invention describes a human genome-derived myosin-protein 1 (hGDMLP-1). The protein and polynucleotide sequences
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30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                     genome-derived myosin-like
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Query Match Best Local Similarity

76.7%; 88.2%;

Score 13.8; Pred. No. 3

8; DB 3e+03;

24;

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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                     protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and
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21-SEP-2000;
27-SEP-2000;
of hGDMLP-1 protein variants having desired phenotypic improvements, at for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specifically of hGDMLP proteins, as specifically concentration, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, for raising antibodies that proteins, or as specific biomolecule capture surface-enhanced laser desorption ionization, myosin-like protein hGDMLP-1
                                                                                                                                                                                                                                                                                                                        The present
                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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myosin; chromosome 22; gene therapy; vaccine;
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l muscle
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2001WO-US00665

2001WO-US00667

2001WO-US00668

2001WO-US00668

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2001US-266860P
                                                                                                                                                                                                                                                                                                                        invention describes a human genome-derived myosin-like
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2000US-234687P.
2000US-236359P.
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disorder; a
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y be used for
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05-FEB-2001;
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21-SEP-2000;
27-SEP-2000;
                                          New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1
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                                                                                                                                                                                                                                                                                                                                                                               muscle; myosin;
skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing a disorder associated with the expression of hGDMLP-1, particular heart and skeletal muscle disorders. hGDMLP-1 is locally chromosome 22. The present sequence represents an oligomer used in screening of the hGDMLP-1 sequence in the exemplification of the presents.
                         Disclosure;
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30-JAN-2001;
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; myosin; chromosome 22; gene therapy; vaccine;
al muscle disorder; amplicon; screening; ss.
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2001WO-US00663.
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2001WO-US00670
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2001WO-US00661.
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2000US-236359P
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88.2%;
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heart disease;
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The present

protein

1 (hGDMLP-1).

The protein describes

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human genome-derived myosin-like and polynucleotide sequences of

invention

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RESULT 9
ABN05560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption constation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                       04-OCT-2000;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                    Human; genome-derived myosin-like protein 1; GDMLP-1;
muscle; myosin; chromosome 22; gene therapy; vaccine;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
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           (AEOM-)
                                                                                                                                                                                                                                                                        25-MAY-2001;
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           AEOMICA
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                                                                                                                                                                                                                                                                                                                                                                                        muscle
                                                    2000US - 207456P.
2000US - 234687P.
2000US - 234589P.
2000CB - 0024263.
2001WO - US00661.
2001WO - US00663.
2001WO - US00664.
2001WO - US00665.
2001WO - US00665.
2001WO - US00665.
2001WO - US00666.
2001WO - US00667.
2001WO - US00667.
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                                        2001US-266860P
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-mer scanning SEQ
                                                                                                                                                                                                                                                                                                                                                                                   chromosome
disorder; a
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88
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Pred. No. 3
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3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                    heart disease;
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characterise
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incoming of the hopping of the hopping of the hopping of the hopping of the present sequence in the expression of the hopping of hopping of hopping the protein variants having desired phenotypic improvements, and for expressing the proteins. The hopping of hopping improvements and the used as immunogens to raise antibodies that specifically recognise hopping. The hopping is that specifically recognise hopping in the proteins, as standards in assays used to determine the concentration and/or amount specifically of hopping proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hopping production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hopping a disorder associated with the expression of hopping a disorder associated with the expression of hopping. The present sequence represents an oligomer used in the sparticular heart and skeletal muscle disorders. hopping-1 is localised to chromosome 22. The present sequence in the exemplification of the present
  Query Match
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Matches 15
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                                                                              Sequence 25
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proteins, or as specific biomolecule capture p
surface-enhanced laser desorption ionization,
myosin-like protein hGDMLP-1
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                    Similarity
                                                                              BP; 6 A; 7 C; 10
  Conservative
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                  76.7%;
88.2%;
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                      Pred. No.
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                                     Score 13.8;
  Mismatches
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RESULT 1
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27-SEP-2000;
04-OCT-2000;
30-JAN-2001;
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skeletal muscle disorder; amplicon; screening;
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muscle; myosin; chromosome 22; gene therapy; vaccine;
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2000US-207456P.
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2000US-236359P.
2000GB-0024263.
2001WO-US00661.
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RESULT 11
ABN05562
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30-JAN-2001;
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30-JAN-2001;
         Human; genome-derived myosin-like protein 1; GDMLP-1; muscle; myosin; chromosome 22; gene therapy; vaccine; skeletal muscle disorder; amplicon; screening; ss.
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                                                                Human GDMLP-1
                                                                                            29-MAY-2002
                                                                                                                                              ABN05562 standard; DNA;
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2001WO-US00669
2001WO-US00669
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2001WO-US00663.
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in electronic i
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                         heart disease;
                                    hGDMLP-1; heart;
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26-MAY-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                         substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the
                           N.B. The sequence data for this patent did not specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequence.
                                                                                                                                                                                                                                                                                                            hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering
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30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins, or as specific biomolecule capture probes for
surface-enhanced laser desorption ionization, comprises
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                                                                                invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEOMICA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID 5554; 214pp; English.
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2001WO-US00662.
2001WO-US00663.
                                                                                             the hGDMLP-1 sequence in the exemplification of
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2001WO-US00667.
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2001WO-US00665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for raising antibodies that recognize hGDMLP-1
A; 6 C; 10 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR,
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Matches Query Match

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                                                                                                     ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 2. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present
                                                                                                                                                                                                                                                                                   hgDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hgDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hgDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hgDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hgDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hgDMLP proteins, as specific blomolecule capture probes for surface-enhanced laser desorption
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30-JAN-2001;
30-JAN-2001;
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21-SEP-2000;
27-SEP-2000;
                           N.B. The sequence data for this patent did not specification, but was obtained in electronic f
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muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin-like protein hGDMLP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, for raising antibodies that proteins, or as specific biomolecule capture proteins of a surface-enhanced laser desorption ionization, myosin-like protein hGDMLP-1
                                                                                  invention.
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  ftp.wipo.int/pub/published_pct_sequence
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;; myosin; chromosome 22; gene therapy; va
.al muscle disorder; amplicon; screening;
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probes for
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vaccine;
                        : form part of the printed format directly from WIPO
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RESULT 13
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the
                                                                                                                                                                                                                                                                                                                               Gu
                                                                                                                                                                                                                             New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human
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skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                The present
                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                  myosin-like
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                                                                                                                                                                                  SEQ
                                                                                                                                                invention describes a
                                                                                                                                                                                                              protein
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Pred. No. 3e
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                                                                                                                                                                                English.
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                                                                                                                                                human genome-derived myosin-like
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therapy; vaccine;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                           Human; antisense; SR-cyp; Clk-associated RS cyclophilin; inflammation; hyperproliferative disorder; cancer; prophylaxis; infection; therapy; tumour; CARS-cyp; phosphorothicate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human SR-cyp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed ification, but was obtained in electronic format directly from WIPO
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88.2%;
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Pred. No. 3
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RESULT 15
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding human SR-cyp (Clk-associated RS cyclophilin) acid molecule encoding human SR-cyp is also referred to as CARS-cyp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antisense compounds targeted to nucleic acids encoding SR-cyp, Clk-associated RS cyclophilin for modulating the gene expression and treating hyperproliferative disorders such as cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-)
                          31-MAY-2001
                                                                                                                                                                   Single nucleotide polymorphism; SNP; heart disease; paternity testing; for
                                                                                                                                                                                                         SLC1A6 polymorphism containing DNA fragment #156
                                                                                                                                                                                                                                                               AAH62255;
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                                                  WO200138576-A2
                                                                                                      Variation
                                                                                                                                            Homo sapiens
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SPRING HARBOR LAB
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Pred. No. 4.4e+03;
0; Mismatches 1;
                                                                           "single nucleotide polymorphism"
                                                                                                                                                                      forensic
                                                                                                                                                                               human;
                                                                                                                                                                    science;
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SR-cyp.
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17-NOV-2000; 2000WO-US31639

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Matches 14; Conserva
                                                                                                                                                                                                                                                     DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 42; 80pp; English.
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                                                                     2001-367705/38.
                                                                                                                                               Conservative
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93.3%;
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                                                                                                                                             Score 13.4; DB 22;
Pred. No. 4.4e+03;
0; Mismatches 1;
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Post-processing: Minimum Match 0%
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2: /cgn2_6/ptodata/1,

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US-08-004-552-2
US-08-687-080-24
US-08-687-080-24
US-09-946-239-5
US-09-936-599-10
US-09-936-599-10
US-09-936-639A-26
US-08-661-155B-12
US-08-661-155B-12
US-08-611-155B-12
US-08-611-155B-12
US-08-611-155B-12
US-08-611-155B-15
US-09-161-244-26
US-09-183-931-6
US-09-183-931-6
US-09-183-931-6
US-09-183-931-5
US-09-75-160-15
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6, Appl
19, Appl
255, Appl
5, Appl
37, Appl
37, Appl
37, Appl
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24, Appl
24, Appl
24, Appli
5, Appli
5, Appli
10, Appl
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68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9	68.9
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US-08-178-019-5	US-08-377-503-6	US-08-377-503-5	US-08-976-288A-90	US-08-134-346A-45	US-08-129-930B-90	US-09-045-940-34	US-08-819-037-34	US-08-320-982-34	US-08-314-596-34	PCT-US92-10792-23	US-09-366-627A-9	US-08-660-561A-10	US-08-523-125-10	US-08-660-561A-7	US-08-523-125-7	US-09-200-232-4	US-09-455-960-14
5	6,	Sequence 5, Appli	Sequence 90, Appl	Sequence 45, Appl	Sequence 90, Appl	•	_	Sequence 34, Appl	•	Sequence 23, Appl	Sequence 9, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 4, Appli	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-08-004-552-2/c
                                                                                US-08-004-552-2
  Query Match
Best Local S
Matches 14
                                                                                                                                                                                                              TELEFAX: (415) 398-3249
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5482836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/004
FILING DATE: 19930114
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Karen S.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                            MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cantor, Charles R.
APPLICANT: Ito, Takashi
APPLICANT: Smith, Cassandra L.
TITLE OF INVENTION: DNA PURIFICATION BY TRIPLEX-AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ZIP: CA 94111
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CITY: San Francisco
STATE: California
                                                                                                 OTHER INFORMATION: /note-
                                                                                                                     NAME/KEY: misc_feature LOCATION: 1..27
                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                    74.48;
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Score 13.4; DB 1;
Pred. No. 5.2e+02;
0; Mismatches 1;
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US-08-687-080-24/c
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US-08-592-126-24/c
                                                                       Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory
TITLE OF INVENTION:
                                                                                                                             Sequence 24, Application US/08687080 Patent No. 5965427
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                    Best
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Patent No. 5821
                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/592
FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gregory TITLE OF INVENTION: TITLE OF INVENTION:
   CITY:
                                                                                                                                                                                                                     17 AGAGAGAGAGGAG 5
                                                                                                                                                                                                                                                                                   Local Similarity les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
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Palo Alto
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821091
              350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                     Conservative
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                                                              Human RAD50 Gene and Methods of Use Thereof 175
                                                                                             Dolganov
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Pred. No.
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7.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 13; Conserv
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APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 36.15
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELEPHONE: (445) 324-0880
TELEPHONE: (445) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: DOWER,
APPLICANT: BARRET'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO:
                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                              ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                     APPLICANT: GALLOP, MARK A
APPLICANT: NEEDELS, MICHAEL C
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                     STATE: CALIFORNIA

CALIFORNIA

ON TOWNSEND

STATE: CALIFORNIA

CALIFORNIA
            APPLICATION NUMBER: US
FILING DATE: 19920916
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AGAGAGAGAGGAG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                        , Application US/07946239 5770358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I: 22 base pairs
nucleic acid
                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                 BARRETT,
                                                                                                                                                                                                                                                                                                                                                                                                     DOWER, WILLIAM J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                  US/07/946,239
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Pred. No.
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                                                                                     #1.25
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; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-151-467-5
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US-09-151-467-5
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US-07-946-239-5
        Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US/07/
APPLIING DATE: 1992-09-16
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION UNUMBER: 30.22
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARRETT, RONALD W
APPLICANT: GALLOP, MARK A
APPLICANT: NEEDELS, MICHAEL C
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TOWNSEND AND TOWNSEND STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 23 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER: 11509-36-1
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6140493
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                                                                                                                                                         23 base pairs
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          Conservative
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     72.2%; Score 13;
100.0%; Pred. No.
tive 0; Mismatc
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        Mismatches
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DB 3; 1, 2, 3, 7,8e+02; 0;
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RESULT 7
US-09-256-838-5
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; MOLECULE TYPE:
US-09-036-599-10
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US-09-036-599-10
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                                                                                                            Sequence 5, Application US/09256838 Patent No. 6416949 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036 FOR FILING DATE:
CLASSTPTT
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APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICANT: Gallop, Mark A.
TITLE OF INVENTION: Method of
TITLE OF INVENTION: Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
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             BARRETT, RONALD W
GALLOP, MARK A
MEEDELS, MICHAEL C
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
COLLECTIONS OF OLIGOMERS
NUMBER OF SEQUENCES: 16
                                                                                              APPLICANT: DOWER, WILLIAM J
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o. 6143497
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100.0%; Pred. No.
rative 0; Mismatcl
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Collections of Oligomers
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND

1 MARKET PLAZA, STEUART TOWER, SUITE 2000

CITY: SAN FRANCISCO STATE: CALIFORNIA

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GENERAL INFORMATION:
APPLICANT: DOWER, WILLIAM J
APPLICANT: BARRETT, RONALD W
APPLICANT: GALLOP, MARK A
APPLICANT: NEEDELS, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND AND TOWNSEND
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                               APPLICANT: NEEDELS, MICHAEL C
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                  APPLICATION NUMBER: POFILING DATE: 19920916 CLASSIFICATION: 435
                                                                                                                                                                                                                COUNTRY:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/256,838
FILING DATE: 24-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-36-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                  CALIFORNIA
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                                                                                          PatentIn Release #1.0,
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INFORMATION:
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Pred. No.
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                                                                                            Version
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. 7.8e+02;
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                                                Matches
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                 TELEFAX: (626) 795-6321 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COASSIN, PETER J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUC
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Wind SOFTWARE: Corel WordPe CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                                                                                                                              TYPE: nucleic acid
                                             Local Similarity es 13; Conserv
                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 20, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08 FILING DATE: May 28, 1997
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4 AGAGAGAGAGGAG
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TYPE: NUCLEIC ACID
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5981185
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225 South Lake A
                                             72.2%; Score 13; DB ilarity 100.0%; Pred. No. 8e Conservative 0; Mismatches
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Pred. No.
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US-08-560-313A-8
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                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-NOV-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1
                                                                   STREET: 50.
STREET: 50.
CITY: Hayward
CTATE: Callfornia
                                                                                                                                                   APPLICANT: Sydney Brenner TITLE OF INVENTION: DNA EXNUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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CTTY: Hayward
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                                                                                                                                                                                                                                                                                                                            11
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REFERENCE/DOCKET NUMBER: sstlus
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OPERATING SYSTEM:
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US FILING DATE: 17-NOV-95
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MEDIUM TYPE: 3.5 inch diskette
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 nucleotides
                                                                                                                     E: Stephen C. Macevicz, Lynx Therapeutics, Inc
3832 Bay Center Place
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Pred. No.
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hes 0;
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RESULT 12
US-08-916-120A-14
; Sequence 14, Application US/08916120A
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JS-08-916-120A-14
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Best Local :
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                                                                                   TELEFAX: (510) 670-93
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510) 670-930 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                              REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 811-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Wo
CURRENT APPLICATION DATA:
                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        FILING DATE: 05-MAR-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
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ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,28
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                       STRANDEDNESS:
                                                                                                                                                                                                        APPLICATION NUMBER: 08
FTI.TNG DATE: 05-MAR-96
                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 22-AUC
CLASSIFICATION: 43
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            TOPOLOGY:
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                                                       LENGTH:
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                                     nucleic acid
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                                                       43 nucleotides
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                                                                                                                   (510)
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19
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100.0%;
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Pred. No.
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RESULT 14
US-09-161-244-26/c
Sequence 26, Application US/09161244
Patent No. 6004814
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US-08-389-360-6/c
                          GENERAL INFORMATION:
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                                                                                                                                                                                                      Query Match
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APPLICATION NUMBER: 08/196,630
FILING DATE: February 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/079,110
FILING DATE: June 17, 1993
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATLICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08389360 Patent No. 5877017
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Best Local
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 APPLICANT:
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APPLICANT: van de
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                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,360
FILING DATE: Herewith
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TITLE OF INVENTION: ISOLATED PEPTIDE WHICH FORMS COMPLEXES
TITLE OF INVENTION: WITH MHC MOLECULE HLA-CW*1601 AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THE NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                         17
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                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pasqualini, Pa
REGISTRATION NUMBER:
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Bennett,
Cowsert,
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805 Third Avenue
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C. Frank
Lex M.
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87.5%;
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100.0%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mb storage diskette
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ພາດ. 9.6e+02;
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US-09-038-328-6/c
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CURRENT APPLICATION NUMBER: US/09/161,244
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 26
LENGTH: 18
 Matches
                Query Match
Best Local Similarity
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Best Local (
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APPLICANT: Van der Bruggen et al.
TITLE OF INVENTION: ISOLATED PEPTIDE WHICH FORMS COMPLEXES
TITLE OF INVENTION: WITH MHC MOLECULE HLA-Cw*1601 AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                        PILING DATE:
PROF APPLICATION DATA:
PRICATION UMBER: 08/079,110
PRILING DATE: June 17, 193
ATTORNEY/AGENT INFORMATION:
NAME: PASQUAIINI, PATTICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET MOMBER: LUD 53:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18F0FAMTION:
TELECOMMUNICATION 18F0FAMTION:
TELECOMMUNICATION 18F0FAMTION:
                                                                                                                                                                        TELEPHONE: (212) 688-92
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch 1.44
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                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS,
OPERATING SYSTEM:
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                   Score 12.8; DB 3; Pred. No. 9.6e+02;
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1: /cgn2_6/ptodata/1/pubpna/pi
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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55540 Ap

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	Sequence 5557, Ap Sequence 11122, A Sequence 11123, A Sequence 11125, A Sequence 11125, A Sequence 11126, A Sequence 11127, A Sequence 11128, A Sequence 11129, A Sequence 11129, A Sequence 91, Appl Sequence 925, Appl Sequence 225, Appl Sequence 53, Appl Sequence 625, Appl Sequence 625, Appl Sequence 742, Appl Sequence 1169, Appl Sequence 167, Appl Sequence 2617, Appl Sequence 2617, Appl Sequence 2621, Appl Sequence 2621, Appl Sequence 2621, Appl Sequence 2621, Appl Sequence 6231, Appl Sequence 6231, Appl Sequence 6231, Appl	

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RESULT 2
US-09-866-108-2619
Sequence 2619, Application U
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT ETLING DATE: 2001-10-02
FRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3925
LENGTH: 19
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; ORGANISM: Glycine
US-09-969-373-3925
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
APPLICANT:
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HANZEL,
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 David
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RESULT 3
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SOFTWARE: Aeoma
SEQ ID NO 2619
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
             APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                             APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
FILE REFERENCE: AEDOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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TYPE: DNA
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APPLICATION NUMBER: PCT/US01/00664
APPLICATION NUMBER: PCT/US01/00664
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                        RANK, David R. CHEN, Wensheng
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NUMBER:
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo s
US-09-866-108-5548
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; Sequence 5549, Application
; Patent No. US20020048800A1
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SEQ ID NO 5548
                                                                                                                                PRIOR PRIOR
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: US 60/236, PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: PCT/US01/00 PRIOR APPLIC
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-25
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
FILE REFERENCE: AEOMICA-7
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                                                                                           OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00668
APPLICATION 2001-01-30
PTTING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00669
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CHEN, Wensheng
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-5549
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Best Local
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
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                                                       ICR APPLICATION NUMBER: PCT/USO1/00666

ICR FILING DATE: 2001-01-30

ICR FILING DATE: 2001-01-30

ICR APPLICATION NUMBER: PCT/USO1/00667

ICR APPLICATION NUMBER: PCT/USO1/00664

ICR FILING DATE: 2001-01-30

ICR APPLICATION NUMBER: PCT/USO1/00668

ICR FILING DATE: 2001-01-30

ICR APPLICATION NUMBER: PCT/USO1/00668

ICR FILING DATE: 2001-01-30

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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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HANZEL, David
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RESULT 6
US-09-866-108-5551
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; ORGANISM: Homo sapiens
US-09-866-108-5550
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SEQ ID NO 5550
LENGTH: 25
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Best Local Similarity
Matches 15; Conserv
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                              PRIOR EILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR EILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NIMBER OF THE PRIOR PRIOR FILING DATE: 2001-02-05
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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APPLICANT: JI, Yongga
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR EILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
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US20020048800A1
                      SEQ ID NOS:
    Aeomica
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PENN, Sharron (
HANZEL, David
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Sequence Listing Engine
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88.2%;
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; ORGANISM: Homo sapiens
US-09-866-108-5552
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                                    Matches
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PRIOR FILING DATE: 2001-02-05
NUMBER OF THE PRIOR FILING DATE: 2001-02-05
                                                                                                                                                        SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 5552
LENGTH: 25
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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TYPE: DN
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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HANZEL, David
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                                    Conservative
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NOS: 15752
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RESULT 9
US-09-866-108-5554
; Sequence 5554, Application U
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-5553
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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SOFTWARE: Aeomica Sequ
SEQ ID NO 5553
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Best Local (
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
FILE REFERENCE: AEOMICA-7
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-25
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Pred. No. 5
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US-09-866-108-5555
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LENGTH: 25
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                    APPLICANT: GU, Yizhong
APPLICANT: JI, Yongga
APPLICANT: PENN, Shar
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                       APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED
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CURRENT FILING DATE: 2001-05-25
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 60/266,860
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
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PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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NUMBER: US 60/234,687
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-5555
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US-09-866-108-5556
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SEQ ID NO 5555
LENGTH: 25
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Best Local
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 0000-10-04
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CURRENT FILING DATE: 2001-05-25
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: PCT,
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APPLICANT: JI, Yongga
APPLICANT: PENN, Shar
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                                   PRIOR FILING DATE: 2001-01-30
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PENN, Sharron
HANZEL, David
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Pred. No. 56
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RESULT 12
US-09-864-761-18548
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LENGTH: 25
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                 PRIOR APPLICATION I
                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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88.2%;
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Pred. No. 5
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; ORGANISM: Glycine max; OTHER INFORMATION: Clone ID: US-09-878-574-7158
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                                                                                                                                     CURRENT APPLICATION NÜMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 7158
LENGTH: 88
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7158, Application US/09878574 Patent No. US20020110548A1
    Matches
                  Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                             APPLICANT: Byrum, Joseph R.
APPLICANT: Lia Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: NOTHER INFORMATION: EOTHER INFORMATION: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4911;
SOFTWARE: Annomax Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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APPLICATION NUMBER: PCT/US01/00661
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  l Similarity
13; Conserv
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NN: EXPRESSED IN LUNG, SIGNAL = 2.9

NN: EXPRESSED IN BRAIN, SIGNAL = 2.9

NN: EXPRESSED IN BY474, SIGNAL = 2.1

NN: EXPRESSED IN HOLTT LIVER, SIGNAL = 2.7

NN: EXPRESSED IN HEL100, SIGNAL = 2.4

NN: EXPRESSED IN HEL100, SIGNAL = 2.4

NN: EXPRESSED IN BONE MARROW, SIGNAL = 3.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9

NN: EXPRESSED IN HELA, SIGNAL = 2

NN: EXPRESSED IN HELA, SIGNAL = 2

NN: EXPRESSED IN HELA, SIGNAL = 3.9

NN: EXPRESSED IN HELA, SIGNAL = 2

NN: EXPRESSED IN HELA, SIGNAL = 3.9

NN: EXPRESSED IN HELA, SIGNAL = 2.00e-02

NN: NT HIT: U80017.1, EVALUE 8.00e-13
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: EXPRESSED IN HEART

: EXPRESSED IN LUNG,

: EXPRESSED IN BRAIN,

: EXPRESSED IN BT474,

: EXPRESSED IN ADULT
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                  Score 13;
Pred. No.
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Pred. No. 8
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    Mismatches
  DB 10; I
1.3e+03;
hes 0;
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3.5e+02;
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                                     Length 88;
  Indels
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RESULT 14 US-09-969-373-205/c 밁

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GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Roger J.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US/0754,853

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-01

PRIOR APPLICATION NUMBER: US/760,427

PRIOR APPLICATION NUMBER: US/760,427

PRIOR APPLICATION NUMBER: US/760,768

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 4593
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; LENCTH: 99
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-205
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GU, Yizhong
APPLICANT: JI, Yongga
APPLICANT: PENN, Shar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
OR APPLICATION NUMBER: PCT/US01/0064
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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PENN, Sharron G.
HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANK, David R.
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; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2618
Search completed: November Job time: 85 secs
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                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/0062
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2000-09-21
PRIOR PHILOR DATE: 2001-02-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 18752
                                                                                                                                          Matches
                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                    Match 71.1%;
Local Similarity 87.5%;
les 14; Conservative
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Perfect score:
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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length: 100
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gb_est2:*
gb_htc:*
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em_gss_pro:*
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gb_gss:*
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ORGANISM RESULT 1 AZ647872 COMMENT REFERENCE ACCESSION DEFINITION Locus TITLE AUTHORS JOURNAL plasmid inserts
Unpublished (2000)
Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical i Rm. 308, Biomedica 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 79)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mandel whole genome scaffolding with paired end reads from 10kb AZ647872 79 bp DNA linear GSS 14-DEC-200 IN0514C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0514C10 R, DNA sequence. Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Mus musculus GSS A2647872.1 GI:11779772 house mouse Genome Center Weiss Polymers Research Bldg., 20 ŝ 2030 GSS 14-DEC-2000 . . SLC, G

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AZ647872 1M0514C10 AI955060 wg60c05.x AL227155 Tetraodon AZ952772 2M0217B14 AI697998 tq14e10.x AZ649857 1M0519008

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                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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www-bio.lln1.gov/bbrp/image/image.html
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                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be Councilled the Land Councilled Council
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                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC1M0514C10"
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/strain="C57BL/6J"
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Pred. No. 5.2e+03;
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                                                                                               This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                 Submitted (12-APR-2000)
                                                                                                                                                                                                                                             Genoscope.
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                                                                                                                                                                                                                                                                                                                                                         Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis DNA sequence
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Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                        Direct Submission
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
39 a 16 c 27 g 13 t
/db_xref="taxon:99883"
                                                                                 Location/Qualifiers
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/clone_lib="NCI_CGAP_GC6"
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. 8.5e+03;
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RESULT 4
AZ952772/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Frax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0217 row: B column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 95)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2M0217B14R Mouse 10kb plasmid UUGC2M library Musclone UUGC2M0217B14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ952772.1 GI:13823999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 95.
Location/Qualifiers
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          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gl14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="211H19"
/clone_lib="G"
/note="Genoscope sequence ID : COAG211CD10SP1-end :
PUC-Ori"
                                                                                                                                                                                                                                         musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0217B14"
/clone_110="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                    /lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                           /sex="Female"
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BASE COUNT
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Best Local
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4 AGAGAGAGAGGAGCC
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46 bp mRNA linear EST 14-DEC tq14el0.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2208810 similar to TR:Q07611 Q07611 PROLINE-RICH PROTEOGLYCAN PRPG2.; contains TAR1.b2 MSR1 repetitive element; mRNA sequence. A1697098
                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality Insert Length: 1168 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNLwww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 46)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
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                                           Conservative
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                                                                                                                                                 ø
                                                                                                                                                                                                                                           /clone="IMAGE:2208810"
/clone_lib="NCI_CGAP_Ut3"
/tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="pHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #:
                                                                                                                                                                    11541-018
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                          74.4%;
93.3%;
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Pred. No.
                                                          Score 13.4; DB 9;
Pred. No. 2.9e+04;
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                                                                           Length 46;
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                                      0,
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                                      Gaps
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11 AGAGAGAGAGGCGCC

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KEYWORDS
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AZ649857/c
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Insert Length: 10000 Std Erro
Plate: 0519 row: O column: 08
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Fax: 801 585 7177
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                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AFT2970721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and the profession of the sheared manual transfer of the sh
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                                                                                                                                                                                                                                                                                               /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0519008"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
                                                                                                                                                            74.4%;
93.3%;
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Pred. No. 2.9e+04;
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                                                                                               AZ996539 54 bp DNA linear GSS 27
2M028ZP14R Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M028ZF14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Mus musculus
                                          GSS
                                                             AZ996539
AZ996539.1 GI:13867766
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                      house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. Fatima Bonaldo.
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/db_xref="taxon:9606"
/clone="IMAGE:1501937"
/clone=1ib="NCI_CGAP_Kid3"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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J3490F Human fetal heart,
clone J3490 5' similar to
N85423
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Insert Length: 10000 Std Error: (
Plate: 0282 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
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(bases 1 to 54)
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801 585 7177
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNPA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0282F14"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                      74.48;
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                                                                                                                                                                                                                                                                                                                                    Score 13.4; DB 17;
Pred. No. 3.1e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Std Error: 0.00
                                                                                                                  75 bp mRNA linear
Lambda ZAP Express Homo s
REPETITIVE ELEMENT, mRNA
                                                                                                                                                                                                                                                                                                                                                                      Length 54;
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JOURNAL
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KEYWORDS
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4 AGAGAGAGAGGAGCC 18
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                                            Medicago Genome Initiative accession:
Insert Length: 884 Std Error: 0.00
Plate: 013 row: B column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                         The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK Tel: 580 221 7325
                                                                                                                                                                                                                                                                                                                             On Jul 14, 2000 this sequence version replaced gi:9197847. Contact: Harrison MJ
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                  Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF013B03PL1F1025 Phosphate starved clone NF013B03PL 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: GAAATTAACCCTCACTAAAAGGG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brigham and Women's Hospital
Harvard Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Liew CC
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Liew, C.C.
                                                                                                                                                                                                       Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 6179750995
                                                                                                                                                                          Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                      Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 84)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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a 4 c 36 g 2 t
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/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/organism="Medicago truncatula"
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93.38;
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leaf Medicago truncatula cDNA
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BM302259/c
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TITLE
Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nours NaCI treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCA040E10 < mRNA sequence.

BM302259
                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014,
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An expressed sequence tag database Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                        Plate: 040 row: E of primer: T3 20mer
                                                                                                                                                                                                                                                                                                                                                         FORWARD: T3 20mer
BACKWARD: T7 21mer
                                                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                            Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cushman, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               common iceplant.
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                                                                                                                                                                                                                                                                                                       quality sequence stop:
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29 c 11 g 24 t
                                                                  /note="Vector: Lambda Uni-Zap XR,
EcoRI; Site_2: XhoI"
27 c 12 g 36 t
                                                                                                                                                          abundant transcripts"
                                                                                                                                                                        /clone_lib="Ice plant Lambda Uni-Zap XR expression library
, 0 hours NaCl treatment prescreened for removal of highly
                                                                                                                                                                                                                                 /organism-"Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Phosphate starved
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3880"
/clone="NF013B03PL"
                                                                                                                         /dev_stage="six-week-old"
                                                                                                                                           /tissue_type="leaf"
                                                                                                                                                                                                                 /clone="MCA040E10"
 74.4%;
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Pred.
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Pred. No. 3.9e+04;
0; Mismatches 1
 13.4;
No. 4
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SOURCE
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BQ765595
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                                                                                                                        AZ325265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeau; Triticeae; Hordeum.

1 (bases 1 to 97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ765595 97 bp mRNA linear EST 26-JUL-2002 EBro03_SQ007_K13_R root, 3 week, waterlogged, cv Optic, EBro03_Hordeum vulgare cDNA clone EBro03_SQ007_K13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                       GSS.
                                                                                                                                     1M0047006R mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0047006 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Invergowrie, Dundee, DD2 5D
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Dynamics/Computational Biology Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources
Mammalia; Eutheria;
1 (bases 1 to 99)
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                  Mus musculus
                                                                                                        AZ325265.1 GI:10381793
                                                                                                                                                                            AZ325265
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                                                                    house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="EBro03_SQ007_K13"
/clone=11b="root, 3 week, waterlogged, cv Optic, EBro03"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Optic"
/db_xref="taxon:4513"
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29 c 26 g
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                                                                                                                                       gene, mRNA sequence.
AA585224
                                                                                                                                                                          AA585224 100 bp mRNA linear EST KTH157 HTCDL1 Homo sapiens cDNA 5'/3' similar to Myosin
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: O column: 06
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 100)
                                                                                                   EST
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                                                          Homo sapiens
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University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA and transformed into
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27 c 25 g 28 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UUGC1M0047006"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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93.38;
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                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                       University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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23 bp DNA linear GSS 102M0025504F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0025104 F, DNA sequence.

AZ783377

AZ783377.1 GI:12918045
                                                                                                                                       High quality sequence stop: 23
                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0025 row: I column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
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Mammalia; Eutheria; Rodentia;
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Fax: 82-053-955-5327
Email: usohn@bh.kyungpook.ac.kr
Seq primer: M13 Reverse/SK primer:
Location/Qualifiers
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Laboratory of Molecular Biology
Kyungpook National University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sohn, U., Park, D.S., Lee, C.M., M.Y. and Jin, S.W. Human HTCDL1 library cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
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Pred. No. 4.2e+04;
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Search completed: November 9, 2002, 15:35:57 Job time: 2178 secs
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Best Local Similarity
Matches 15; Conserv
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/ Nab_host="E. Coli strain XI10-Gold, T1-resistant, F-"  
// Nab_host="E. Coli strain XI10-Gold, T1-resistant, F-"  
// Note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BI_6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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## SUMMARIES

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SUS	E31253 1447 bp DNA linear PAT 18-JUN-2001
FINITION	Protein having cell calcifying inhibitory activity and gene
	encoding the same.
CESSION	E31253
RSION	E31253.1 GI:13025685
WORDS	JP 1999075871-A/1.
JRCE	unidentified.
DRGANISM	unidentified
	unclassified.
FERENCE	1 (bases 1 to 1447)
AUTHORS	Hiroyasu, I., Yoshinobu, H., Marijio, P., Joel, R. and Helena, E.
TITLE	Protein having cell calcifying inhibitory activity and gene
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Best Local Similarity 100.0%;
Matches 1447; Conservative
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REFER AUT	VERSION KEYWORDS SOURCE ORGANI	ACC E	RESUL AY065 LOCUS	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Дb	Qy	DЬ	γQ	Дb	VΩ	Db	Qy	рь	Qy	Db	Qy	ф	Qy	Db	Qy	Db	Qy	Db	Qy
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Archosauria; Aves; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  1 (bases 1 to 1413)  Iwamoto, M., Higuchi, Y., Koyama, E., Enomoto-Iwamoto, M., Kurisu, K.,	40	spliced.	AYO:	AAGAAA 1447	AAGAAAA 1447	CTGCTCATATGCCTTCCCATCTTGGCACCTACTAAGTGGGGAAAGAAA	TGCTCATATGCCTTCCCATCTTGGCACCTACTACTAAGTGGGGAAAGAAA	CCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCTGCCAG 1380	CCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCTGCCAG 1380	TGAACTTTGTAGCTCCCCATCCCCCTGCTTTGCCCCGTAACCTCATCCAGCTTTTTTGCTG 1320	TGAACTITGIAGCTCCCCATCCCCCTGCTTTGCCCCGTAACCTCATCCAGCTTTTTTTGCTG 1320	TGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACCCCCAGAAGA 1260	TGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACACCCCCAGAAGA 1260	ACAAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCCTCCAGCCTCCAGAATCATCCA 1200	ACAAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCCTCCAGAATCATCCA 1200		CACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGCTATGCCT 1140	CTCGGCGTTGGGGAAAAGCAAAACCTAACATGAACTATGACAAACTCAGCCGTG 1080	CTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTCAGCCGTG 1080	ACTGCATCACCTGGGAGGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGAAGTGG 1020	ACTGCATCACCTGGGAGGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGAAGTGG 1020		GTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCAACTCCA 960	CTCAGTTAGATCCTTATCAGATTCTTGGACCGACCAGCAGCCGTCTTGCAAATCCAGGGA 900	CTCAGTTAGATCCTTATCAGATTCTTGGACCGACCAGCAGCGTCTTGCAAATCCAGGGA 900	CTCAGTCAAAAGCTACCCAACCATCATCTTCAACAGTGCCCAAAACAGAAGACCAGCGTC 840	CTCAGTCAAAAGCTACCCAACCATCATCTTCAACAGTGCCCAAAACAGAAGACCAGCGTC 840		7		CCACTTTTATTTTTCCAAATACATCAGTTTACCCAGAAGCAACGCAAAGAATAACAACAA

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                                                      CCGCGCGTTCCCCAGCAGGACTGGTTATCACAGCCCCCGGCCAGAGTTACCATTAAGATG
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Iwamoto,M., Higuchi,Y., Enomoto-Iwamoto,M., Kurisu,K., Koyama,E., Yeh,H., Rosenbloom,J. and Pacifici,M.
The role of ERG (ets related gene) in cartilage development Osteoarthr. Cartil. 9 Suppl A, S41-S47 (2001)
21535378
11680687
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Transcription factor ERG variants and functional diversification
chondrocytes during limb long bone development
J. Cell Biol. 150 (1), 27-40 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (05-DEC-2001) Oral Anatomy and Developmental Biology, Osaka University Faculty of Dentistry, 1-8 Yamadaoka, Suita, Osaka University Faculty of Dentistry, 1-8 Yamadaoka, Suita, Osaka University
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Iwamoto, M., Higuchi, Y.,
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skmsprpqodwlsqpparvilkmechpnqvngsrnspddcsvakggkaysssdnvgm
nygsyneekhipppnmtnerryippadptlmstdhvrgmlenavkeyglpdddille
QNIDGKELCKWTKDDEQRLTPSYNADILLSHLHYLRERGATFIPPNTSYYPEANGRIT
TRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLA
NPGSGQIQLWQFTLELLSDSSNSNCITWEGTNGEFKNTDPDEVARRWGERKSKPNMNY
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/db_xref="taxon:9031"
37...1392
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YHAHPQKMNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPAAHMPSHLGTY
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/protein_id="AAL40889.1"
/db_xref="GI:17887441"
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RESULT E31254 LOCUS

DEFINITION

E31254 1528 bp DNA linear Protein having cell calcifying inhibitory activity

PAT 18-JUN-2001 and gene

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	CCTACTACTAAGTGGGGAAAGAAAGAAA	1381	В
	ACCTACTAGTGGGGAAAGAAAA 1435	1407	QΨ
1380	GCTGCTCATATGCCTTCCCATC	1321	Db
1406	TGGAGGCATCTACCCCAATACCAGGCTGCCAGCTGCTCATATGCCTTCCCATCT	1347	Ωу
1320	TGCC	1261	B
1346	TTTGCCCGTAACCTCATCCAGCTTTTTTGCTGCCCCTAATCCATACTGGAATTCACC	2	Qy
1260	TACATGAGTTCCTACCATGCACACCCCCAGAAGATGAACTTTGTAGCTCCCCCATCCCCCT	2	В
1286	ACATGAGTTCCTACCATGCACACCCCCAGAAGATGAACTTTGTAGCTCCCCCATCCCC	1227	VΩ
	CAGGCCCTCCAGCCTCCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCC	-	망
1226	AGGCCCTCCAGCCTCACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCC	1167	Qy
1140	TATGACTAAAGTTCATGGTAAACGCTATGCCTACAAATTTGATTTCCACGGAAT	1081	Вb
1166	ATTATGACTAAAGTTCATGGTAAACGCTATGCCTACAAATTTGATTTCCACGGAATCGCT	_	Qγ
æ	AAACCTAACATG	1021	망
1106	AAACCTAACATG	1047	γQ
1020	GGGGAGTTCAAG	961	B
1046	GGGGAGTTO	987	δÃ
960	CTACTGGAGCTT	901	망
986	CTACTGGAGCTTCTGTCGGACAGCTCCAACTCCAACTGCATCACCTGGGAGGGCACAAA	927	γQ
900	GGACCGACCAGCAGCCGTCTTGCAAATCCAGGGAGTGGGCAGATACAGCTATGGCAGTTC	841	밁
926	GGACCGACCAGCAGCCGTCTTGCAAATCCAGGGAGTGGGCAGATACAGCTATGGCAGTT	867	δÔ
840	TCTTCAACAGTGCCCAAAACAGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCTT	781	Вb
866	CTTCAACAGTGCCCAAAACAGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCT	807	Qy
780	GACGAGTCACAGCCATCCCACTCAGTCAAAAGCTACCC	721	В
806	SATCAGCGTGGACGAGTCACAGCCATCCCACTCAGTCAAAAAGCTACCCAACCATC	747	ΨQ
720	GTTTACCCAGAAGCAACGCAAAGAATAACAACAAGGCCAGATTTACCTTATGAGCAAGCG	661	뫄
746	CAAGGCCAGATTTACCTTATGAGCAAGC	687	δ
660	CTGTCACACCTACACTACCTCAGAGAGAGGAGGCCACTTTTATTTTTCCAAATACATCA	601	β
	GAGCCACTTTATTTTTCCAAATACATC	627	VΩ
600	TGTAAAATGACCAAAGATGACTTCCAGAGACTCACGCCGAGCTATAACGCAGATATCCTC	541	밁
626	- i-i	567	Ϋ́
540		481	В
566	atggtcttccagacgtggacatcttgttgttccagaacattgatgggaaagagtt	507	δ
480	GCAGATCCTACGTTATGGAGCACAGACCATGTACGGCAGTGGCTGGAGTGGGCAGTGAAG	421	망
506	ATCCTACGTTATGGAGCACAGACCATGTACGGCAGTGGCTGGAGTGGCCAGTC	447	Qy

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Best Local Similarity 94.7%;
Matches 1447; Conservative
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patent: JP 199075871-A 2 23-MAR-1999;
CHUGAI PHARMACEUT CO LTD, HE TRUSTEES OF THE UNIVERSITY OF
PENNSYLVANIA
OS Unidentified
PN JP 199075871-A/2
PD 23-MAR-1999
PR 23-MAR-1999
PR 18-JUN-1997 US 60/050297 PI
HIROYASU IWANOTO, YOSHINOBU HIGUCHI, MARIJIO PASHIFIKI, PI JOEL
ROZENBUROOM,
PI HELENA E
PC C12P21/02,
PC C12P21/08, C12N15/00, A61K47/02
CC Strandedness: Single;
FH Key
CT Topology: Linear;
FH Key
FF Source

/Organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                       CCAATGAACGAAGAGTTATTGTGCCAGCAGATCCTACGTTATGGAGCACAGACCATGTAC
                                           CCCCGGCCAGAGTTACCATTAAGATGGAGTGTAACCCAAACCAGGTTAATGGGTCAAGGA 300
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E31254
E31254.1 GI:13025
JP 1999075871-A/2.
unidentified.
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C12N15/09, A61K48/00, C07K14/465, C07K16/18, C12Q1/68//A61K38/00
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/organism='Unidentified'
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                   ACTATGACAAACTCAGCCGTGCACTTCGCTACTACTATGACAAAATATTATGACTAAAG 1119
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TTATGGCAAGCACTATTAAGGAAGCATTATCAGTGGTGATGATGAAGACCAGTCCTTGTTTG 120
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95329425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1516)
Duterque-Coquillaud, M.
Direct Submission
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1 (bases 1 to 1516)

1 (bases 1 to 1516)

1 Dhordain, P., Dewitte, F., Desbiens, X., Stehelin, D. and Duterque-Coquillaud, M.
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63. .1499
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GIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALPVTSSSFFAAPNP
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392 c 327 g 339 t
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conlockelckmtkddforltpsynadillshlhylretplphltsdyvkalonsprl
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/db_xref="GI:790440"
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240 ACCATGCACACCCCCAGAAGATGAACTTTGTAGCTTCCCCATCCCCTTGCTTTGCCCGTAA 1200		οv
261 CTCACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCT 1320	.26	ф
80 CTCACCCTCCAGAATCATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCC	18	Qy
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141 ACTATGACAAACTCAGCCGTGCACTTCGCTACTACTACTATGACAAAAATATTATGACTAAAG 120	<b>4</b> C	
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CAAAACAGAAGACCAGCGTCCTCAGTTAGATCCTTATCAGATTCTTGGACCGACC	N	δŌ
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Rattus norvegicus VESP14
specific protein 14, comp
AB031088
AB031088.1 GI:15128488
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-AUG-1999) Tomomi Aoki, Taisho Pharmaceutice Ltd., Medicinal Research Laboratories, Molecular Biology 1-403, Yoshino-cho, Omiya, Saitama 3308530, Japan (E-mail:s17704@ccm.taisho.co.jp, Tel:048-663-1111, Fax:048-652-7254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular endothelial cell specific protein 14. Rattus norvegicus liver cDNA to mRNA. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Imammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Aoki, T., Toyoda, H.,
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                                                                            /product="vascular endothelial cell specific protein 14"
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QNIDGKELCKMTKDDFQRLTPSYNADJILSHLHYLFETPLPHLTSDDVDKALQNSPRL
MHARNTTLPYEPPRRSTMTGHSHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTS
SRLANPGSGQIQLMQFFLELLSDSSNSNCITMEGTNGEFMXTDDDEVARRWGERKSKP
NMNYDKLSRALRYYYDKNIMTKVHGKRYAKFDFHGIANALQHPPPESSLYKYPSDLP
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norvegicus VESP14 mRNA for
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Toyoda, H.,
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63. .1430
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/codon_start=1
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Rao,V.N., Papas,T.S. and Reddy,E.S.
erg, a human ets-related gene on chromosome splicing, polyadenylation, and translation Science 237 (4815), 635-639 (1987)
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SSDYGGTSKMSBRVPGDFRSAWTGHGHPPPGSKAAQPSBTVPKTEDQRPQLDPY
ONSTLLEON INCOME FRANCHENTEN FRANCHERT WEGTREFKWTDPDEVARRW
GERKSKPNMVDKLSRALRYYYDKNIKMTKVHGKRYAYKFDEHGIAQALQPHPPESSLY
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ERG gene; ti
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PYMSSYIAHPQKMNEVAPHPPALPVTSSSFFAAPNAYWNSPTGSIYPNTRLPASHMSS
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                                                                                                                                                                                                                                                                                                                     Submitted (16-OCT-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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Ozawa, R., Noguchi, H., Taylor, T.D.
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                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                               Ozawa,R., Noguchi,H., Taylor,T.D., Takeda, Sakaki,Y.
Direct Submission
Submitted (16-OCT-2001) Masshira Hattori,
                                                                                                                                                                                                                                                                     Published Only in Dat 2 (bases 1 to 2209)
                                                                                                                                                                                                                                                                                                            Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  transcript variant AB073080
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/note="homolog
variant 3"
                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="16"
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                         /gene="Erg"
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                                        TACAACTAGGCCAGATTTACCTTATGAGCCTCCCAGGAGATCAGCCTGGACCGGCCACAG
                                                                                                      AGGGGGTGCAGCTTTTATTTTCCCAAATACTTCAGTATATCCCGAAGCTACGCAAAGAAT
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//db_xref="G1:16197545"
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//tanslation="MICTYPDEAAHIKEALSVVSEDOSLFECAYGTPHLAKTEMTASS
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DVDVLLFQNIDGKELCKMTKDDFORLTPSYNADILLSHLYLAETPLPHTSDDVDKA
LQNSPRLMHARNYGGAAFIFPNTSVYPEATQRITTRPDLLPXEPPRRSAWTGHSHLTPQ
SKAAQBSPSAVPKTEDQRPQLDPYQILGPTSSHLANPGSGQIQLMQFTLELLSDSSNS
NCITWEGTNGEEKMTDPDEVARRWGERKSPNNNYDKLSRALRYYYDKNIMTKVHGKR
YAYKFDFHGIAQALQPHPPESSLYKYPSDLPYMGSYHAHPQKMNFVSPHPPALPVTSS
SFFASPMPYWNSFTGGIYPNTTRLPASMPSHLGTYY"
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Location/Qualifiers
                                                                                                                      Direct Submission
                                                                                                                                   Sakaki, Y.
                                                                                                                                              Mus muscullus Erg mRNA
Published Only in Database (2001)
2 (bases 1 to 2133)
Ozawa,R., Noguchi,H., Taylor,T.D.,
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/db_xref="taxon:10090"
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                       /organism="Mus musculus"
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AACAAGGCCAGATTTACCTTATGAGCAAGCGAGGAGATCAGCGTGGACGAGTCACAGCCA
                                    TGCCGACATTCTTCTCTCACATCTCCACTACCTCAGAGAGACTCCCCCTTCCACATCTGAC
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SPDTYGMSYGSYMEEKHYPPPNMTTNERRVIVPAADPTLMSTDHYRQWLEWAVKEYGLL
DVDVLLFQNIDGKELCKMTKDDFQRLTPSYNADILLSHLHYLRETPLPHLTSDDVVRA
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WGERKSKPNNNYDKLSRALRYYYDKNIXMTKYHGKRYAYKFDFHGIAQALQPHPPESSL
YKYPSDLPYMGSYHAHPQKMNFVSPHPPALPYTSSSFFASPNPYWNSPTGGIYPNTRL
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149. 1540
/gene="Erg"
/note="homolog of variant 2"
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Submitted (24-FEB-1998)
National de la Recherche
67084, FRANCE
                                                     Baltzinger, M.
Direct Submission
                                                                                                    Baltzinger,M., Mager-Heckel,A.M. and Remy,P. X1 erg: expression pattern and overexpression during plead for a role in endothelial cell differentiation Dev. Dyn. 216 (4-5), 420-433 (1999) 20099678
                                                                                                                                                                                                                              Xenopus laevis erg gene
AJ224125
AJ224125.1 GI:5420045
ERG gene; transcription
                                                                                                                                                             Xenopodinae; Xenopus.

1 (bases 1 to 1798)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
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Pipidae;
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/db_xref="GI:5420046"
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/db_xref="taxon:8355"
/clone="lambda ZAPII-erg A
/clone_lib="lambda ZAPII"
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1 of 2
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                      ases 1 to 3126)
,E.S., Rao,V.N. and Papas,T.S.
rg gene: a human gene related to the ets oncogene
Natl. Acad. Sci. U.S.A. 84 (17), 6131-6135 (1987)
 Location/Qualifiers
                                                         Eutheria;
                                                                Metazoa;
                                                                                                                          3126 bp
(ets-related)
                                                        Chordata;
Primates;
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                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                        TCGGACAGCTCCAACTCCAACTGCATCACCTGGGAGGGCACAAATGGGGGAGTTCAAGATG
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LRETPLPHLTSDDVDKALQNSPRLMHARNTDLPYEPRRSAWFGHGHPTPQSKAAQPS
PSTVPKTEDQRPQLDPYQILLFDTSSRLANPGSGQIQPLAFELLSDSSNSSZITWEG
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/organism="Homo
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20108585
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Danio rerio.
Danio rerio
Danio rerio
Cherdata; Craniata;
Cherdata; Craniata;
Cherdata; Craniata;
Cherdata; Craniata;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1436)
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Submitted (29-SEP-1999)
Sciences, University of
9PT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                 ETS-domain transcription factor zebrafish embryos Mech. Dev. 90 (2), 237-252 (2000
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to Sharrocks, A.D.
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45. .1400
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                              University Avenue, Toronto Ontario M5G 1X5, CANADA 2 (bases 1 to 1729)
Ben-David,Y., Giddens,E.B., Letwin,K. and Bernstein,A.
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                                                                                                                                                                                                                                                                                                 Erythroleukemia induction by Friend murine insertional activation of a new member of t Fli-1, closely linked to c-ets-1 Genes Dev. 5 (6), 908-918 (1991)
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-MAY-1991) K. Letwin, Samuel Lunenfeld Res
Mount Sinai Hospital, Div of Mol and Developmental Biol
University Avenue, Toronto Ontario M5G 1X5, CANADA
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxon:10090"
/cell_line="CB7"
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/codon_start=1
/product="retrovirus
                               /gene="Fli-1"
                                                           /evidence=experimental
                                                                           /gene="Fli-1"
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 TCTGGCCTCAACAAAAGTCCTCTCCTTGGAGGATCACAGACCATGGGCAAGAACACTGAG
                                                               GTCAAGGAAGACCCTTCTTATGACTCTGTCAGGAGGAGGAGGATGGAACAATAATATGAAC
                                                                                             ACAAGGCCAGATTTACCTTATGAGCAAGCGAGGAGATCAGCGTGGACGAGTCACA----GC
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NSYMDEKNGPPPNMTTNERRVIVPADPTLWTQEHVRQWLEWAIKEYGLMEIDTSFFQ
NMDGKELCKMNKEDFLAATSAYNTEVLLSHLSYLRESSLLAVWTSHFTDQSSRLNVKE
DPSYDSYRGAMNNMNSGLNKSPLLGGSQTMGKNTEQRPQPDPYQILGPTSSRLANK
GSQQIQLWQFLLELLSDSANASCITWBCTNGEFKMTDDDEVARRWGEKKSKPNNYDK
LSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTETSMYKYPSDISYMPSYH
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Sequence 2 :
A36461
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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/dev_stage="ADULTE"
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                                                                                                                                                GAAGTGGCTCGGCGTTGGGGAGAGAGGGAAAAGCAAACCTATGAACATGAACTATGACAAACTC
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Search completed: November 9, 2002, 11:35:56 Job time: 3957.96 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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							<pre>inhibiting activity; protein; arthritis deformans;</pre>						Human secreted pro cDNA encoding Ratt Rat lambda73 cDNA Drosophila melanog Human foetal liver	genome	Probe #1711 used t	bone :	Probe #1653 for ge Human brain expres	foetal			#3705 for g	Human breast cell Human foetal liver	Hum-Fli- #54 encod	Probe #8687 used t Human secreted pro	Probe #17025 used	brain expre	Probe #13618 for q	Human breast cell	Probe #6634 used t Human genome-deriv	Probe #14862 used	Human bone marrow Probe #10865 for q

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(first entry)

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Best Local Similarity 66.5%;
Matches 913; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatmen of Ewing sarcoma and melanoma
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Ews gene; malignant melanoma; hum-fii-1;
printitive peripheral neuroectodermal tumour;
human chromosome 22; ss.
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DB; AAR44556.
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                   GTTGGGATGAACTATGGAAGCTACATGGAAGAGAAGCAT---ATTCCGCCTCCAAATATG
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CC the expression level to an expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in GS; (2) screening (CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from GS, where CC level of expression of the gene is indicative of inflammation, (A5) an inflammation (especially chronic) or in a tissue, CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, CC an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue, M1 is useful for detecting GCA; M2 is useful for CC cresponse in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, M1 is useful for detecting GCA; M2 is useful for CC detecting an inflammation (especially chronic) in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, (e.g. psoriasis, rheumatoid arthritis, CC detecting an inflammation (especially chronic) in a tissue, an allergic cresponse in a subject, exposure of a subject to a pathogen or sterile conflammatory disease, also bacterial infection, viral infection, creperfusion injury, renal creperfusion injur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac reperfusion
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cardiac reperfusion injury; renal reperfusion injury;
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                        The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in t diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                          Nojima F
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27-SEP-2000;
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                 nucleic acid probes for measuring gene expression in a sample deriftrom human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to
                                                                                                                                                                                                                   Claim 4;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1136
                               09-AUG-2001
                                                                                                                                                                               01-FEB-2002
                                                                                                                                                                                                                                           ABA66003
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30-JAN-2001; 2001WO-US00669
                                                            WO200157277-A2
                                                                                                                                                    Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATGAACTTTGTAGCTCCCCATCCCCCTGCTTTTGCCCGGTAACCTCATCCAGCTTTTT
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                                                                                                                                                                                                                                                                                                                      CCCCACCAGCCATATGCCTTCTCATCTGGGCACTTACTACTAA
                                                                                                                                                                                                                                                                                                                                                                                                             TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                TGCTGCCCCAAACCCATACTGGAATTCACCAACTGGGGGTATATACCCCCAACACTAGGCT
                                                                                                                                                 foetal liver single exon nucleic acid probe
                                                                                                                      foetal
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83.7%;
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Best Local S
Matches 438
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         1136
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43
                          GCCAGCTGCTCATATGCCTTCCCCATCTTGGCACCTACTACAA
                                                                                                          TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT
                                                                                                                                                                                                           GAAGATGAACTTTGTAGCTCCCCATCCCCTGCTTTGCCCGTAACCTCATCCAGCTTTTT
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                                                                                                                                                                                   GAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCGTGACATCTTCCAGTTTTTT
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                                                                                                                                                                                                                                                                            438;
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zing gene expression in
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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83.7%;
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liver -
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Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
  1076
                                                                                                                                                                                                                                   measuring human gene expression in a sample derived from human heart. The probes may be used for present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systee.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                         1016
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; cardiovascular disease;
                                                                                                                                                                                                                   specification,
                                                                                                                                                                                                                                                                                                                      The present
                                                                                                                                                                                                                                                                                                                                                                        Single
                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
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                                                                                 956
                                                                                                                          896
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                                                         AGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCAA 955
CCGTGCACTTCGCTACTACTATGACAAAATATTATGACTAAAGTTCATGGTAAACGCTA 1135
                              AGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAAACCTAACATGAACTATGACAAACTCAG 1075
                                                                                                                                                                                                                The sequence data for this patent did no fication, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                             2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                SG,
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; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                        nucleic
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                    invention relates to single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                DK,
                                                                                                                                                                                   114 A; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                           11556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                     26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heart; microarray; vascular system; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                       probes
                                                                                                                                                                                                                                                                                                                                       530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    INC
                                                                                                                                                                                                                                                                                                                                                                                                                Ę
                                                                                                                                                                                   Ç
                                                                                                                                            0;
                                                                                                                                           Score 387; DB Pred. No. 5.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis
                                                                                                                                                                                   G;
                                                                                                                                                                                                                                                                                                                                                                      analyzing
                                                                                                                                                                                   129 T;
                                                                                                                                           DB 22;
5.2e-117;
les 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                            not
                                                                                                                                                                                   0 other;
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format
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                                                                                                                                                              Length
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                      expression
                                                                                                                                                                                                                part of the directly from
                                                                                                                                                               567;
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                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                       human
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RESULT 9

AAK14426/c

ID AAK14426;

XX AC AAK14426;

XX O5-NOV-200

XX DE Human brai

XX Microarray

KW Human; bra

KW Microarray

KW epilepsy;

XX O9-AUG-200

XX O9-AUG-200

XX O4-FEB-200

PR 04-FEB-200

PR 26-MAY-200

PR 27-SEP-200

PR 27-SEP-200

PR 27-SEP-200

PR 27-SEP-200

PR 27-SEP-200

PR 03-AUG-200

XX OMCLE-) MO

XX MOLE-) MO

XX MPI; 2001-

XX WPI; 2001-

XX WPI; 2001-

XX Single exo

PT Single exo

PT Single exo

PT Single exo

PT Single exo

The presen

CC The presen
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                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                              probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1316
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                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGCTGCTCATATGCCTTCCCATCTTGGCACCTACTACTAA 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATGAACTTTGTAGCTCCCCATCCCCCTGCTTTGCCCCGTAACCTCATCCAGCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACACCCCCA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCGCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCATGGGAAGCGCTA
                                                                                                                                                                                                                                                2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCACCAGCCATATGCCTTCTCATCTGGGCACTTACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT
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                                                                                                                                                                                                  exon
                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                   MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                Hanzel
                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                  ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236839.
; 2000US-0236359.
                                                                                                                                                                                                             nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                          IJ
                                                                                                                                                                                                                                                                               DK,
                                                                                                                                                          ŏ:
                                                                                                                                                                                                                                                                                                                   DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                        provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                Chen
                                                                                                                                                       14417; 650pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567
                                                                                                                                                                                                           probes
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                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                           for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe
                                                                                                                                                                                                                                                                                ДR
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO:
                                                                                                                                                                                                           gene expression
                                                                                                                                                       Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe;
                                                                                                                                                       English
                                                                                                                                                                                                           'n
                                                                                                                                                                                                             human
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RESULT 10
AAK40160/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                              1376
                                                                                                                                                                                                                                                                                                                                                                      1316
                                                                                                                                                                                                                                                                                                                                                                                                           1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1136
(MOLE-)
                                                                                                                                                                                                                                                            AAK40160 standard; DNA; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                             30-JAN-2001;
                                                                                                                09-AUG-2001.
                                                                                                                                   WO200157276-A2
                                                                                                                                                                       microarray;
                                                                                                                                                                                   Human;
                                                                                                                                                                                                     Human
                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                          AAK40160;
                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 438; Conserv
                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                      GCCAGCTGCTCATATGCCTTCCCATCTTGGCACCTACTACTAA 1418
                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATGAACTTTGTAGCTCCCCATCCCCCTGCTTTGCCCCGTAACCTCATCCAGCTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCATGTACAAATACCCCATCAGACCTCCCCCTACATGAGTTCCTACCATGCACACCCCCA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCGCCCTCCGTTACTACTATGACAAGAACATCATGACCAAGGTCCATGGGAAGCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGCTA 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCAACTGCATCACCTGGGAGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGA 1015
                                                                                                                                                                                                                                                                                                           CCCCACCAGCCATATGCCTTCTCATCTGGGCACTTACTACTAA
                                                                                                                                                                                                                                                                                                                                                            TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                       GAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCGTGACATCTTCCAGTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAGCTGCATCACCTGGGAAGGCACCAACGGGGAGTTCAAGATGACGGATCCCGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCAGTGGCCAGATCCAGCTTTGGCCAGTTCCTCCTGGAGCTCCTGTCGGACAGCTCCAA
                                                                                                                                                                                                                                                                                                                                                 TGCTGCCCCAAACCCATACTGGAATTCACCAACTGGGGGTATATACCCCCAACACTAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                             bone
                                                                                                                                                                                  bone
MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567
                                                                                                                                                                                                    marrow
                                                                                                                                                                                 marrow
                                                                                                                                                                        cancer;
                 2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                          2000US-0180312
                                                                                             2001WO-US00668
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
DYNAMICS
                                                                                                                                                                                                    expressed
                                                                                                                                                                                expressed exon; gene expression analysis;
                                                                                                                                                                       leukaemia; lymphoma; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                    exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                    probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                    NO:
                                                                                                                                                                                                    14717.
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                                                                                                                                                                                 probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                             164
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RESULT 11
AAI20932/C
ID AAI20
XX AAI20
AC AAI20
XC AAI20
XX 12-OC
XX 12-OC
XX Probe
XX Probe
KW Cervi
XX
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               cervical
                        Probe; human; microarray; gene
                                                                                                                        AAI20932 standard;
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                                                                                                                                                                                   ATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACACCCCCA
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                                                                                                                                                                                                                                                TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT
                                                                                                                                                                                                                                                                                                            GAAGATGAACTTTGTAGCTCCCCATCCCCCTGCTTTGCCCCGTAACCTCATCCAGCTTTTT
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zing gene expression in human
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              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention provides a number of single exon nucleared derived from genomic sequences expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                               for gene expression
                                                                       (first
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83.7%;
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Pred. No. 5.2e-117;
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                         expression;
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an bone marrow -
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                        cervical epithelial cell;
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                                                cervical cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeIa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPO
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                     CTCCAACTGCATCACCTGGGAGGCACAAATGGGGAGTTCAAGATGACAGACCCTGATGA 1015
              GAAGATGAACTTTGTAGCTCCCCCATCCCCCTGCTTTGCCCGGTAACCTCATCCAGCTTTTT
                                                     TGCCTACAAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCCTCCACCCTCCAGAATC
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GAAGATGAACTTTGTGGCGCCCCACCCTCCAGCCCTCCCCGTGACATCTTCCAGTTTTTT
                                                                                  ATCCATGTACAAATACCCATCAGACCTCCCCTACATGAGTTCCTACCATGCACACCCCCA
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zing gene expression in human cervic
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
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83.7%;
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
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TGCTGCCCCTAATCCATACTGGAATTCACCAACTGGAGGCATCTACCCCAATACCAGGCT

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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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CCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGCTA
                                        GGTGGCCCGGCGCTGGGGAGAGCGGAAGAGCCAAACCCAACATGAACTACGATAAGCTCAG
                                                                        AGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTCAG
                                                                                                                  AGGCAGTGGCCAGATCCAGCTTTGGCAGTTCCTCCTGGAGCTCCTGTCGGACAGCTCCAA
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2000US-0207456.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
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83.7%;
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.2e-117;
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523

896 AGGGAGTGGGCAGATACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCAA 955

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Best Loc Matches

al Similarity 438; Conser

Conservative

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Score 387; DB Pred. No. 5.2e 0; Mismatches

DB .2e-117;

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Gaps

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Sequence

567

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114 A; 124 C; 26.7%; 83.7%;

200

G; 129

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0 other;

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CC nucleic acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung, comprising (a) contacting the array with CC a collection of detectably labeled nucleic acids derived from human lung (measuring the label detectably bound to each probe of CC (a) algorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, CC (a) algorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC in tissues and/or cell types using hybridisation to a single exon of cexpression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one CC of 12011 sequences, mentioned in the specification, or encoded by the CC purpossion analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (CCDP), interstitial lung disease (ILD), familial idiopathic pulmonary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, candinary disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon con both one neading frame of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                    probe open reading frame of the invention.
Note: The sequence data for this patent did not for of the printed specification, but was obtained in format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4;
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632368.
; 2000US-0234686.
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                                              exon nucleic acid probes, sample derived from human nucleic acid probes -
  listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression;
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US-09-784-316-3
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61 TTGGGATGAACTATGGAAGCTACATGGAAGAGAAACCA: 	41 CCCCGGCCAGACTTACCATTAAGATGGAGTGTAACCC  [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	21 AGTGTGCCTACGGATCGCCCCACCTTGCAAAGACAGA 81 AATATGGGCAAACATCAAAGATGAGCCCGCGCGTTCCC 	1 GAATTCCGCGAACGAATAATTATTATTATTAGCAATTATTAGI	0%; Score 1447; D 0%; Pred. No. 0; 0; Mismatches	RESULT 1  US-08-878-177-1  US-08-878-177-1  Sequence 1, Application US/08878177  Patent No. 6294354  GENERAL INFORMATION:  APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 500;  TITLE OF INVENTION: Cell Calcification Suppress;  TITLE OF INVENTION: the Proteins  FILE REFERENCE: chugai seiyaku kabushiki kaisha;  CURRENT APPLICATION NUMBER: US/08/878,177;  CURRENT FILING DATE: 1997-06-18;  NUMBER OF SEQ ID NOS: 7  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 1  LENGTH: 1447  TYPE: DNA  ORGANISM: C-11 gene, c-erg gene w/ deletion, 0	ALIGNM	38.8 2.7 2428 3 US-09-009-913-6 38.8 2.7 2498 3 US-09-009-913-10 35.2 2.4 2432 2 US-08-469-4412A-3 35.2 2.4 2432 4 US-09-046-578-1 33.4 2.3 1212 3 US-08-878-177-3 32.6 2.3 1528 4 US-08-878-177-3 32.6 2.3 1528 4 US-08-878-177-3 32.6 2.3 1528 4 US-08-878-177-3	58.2 4.0 5510 3 US-09-009-913-3 58.2 4.0 5667 3 US-09-009-913-4 55.2 3.8 2975 1 US-08-368-281-3 55.2 3.8 3240 1 US-08-368-281-3 53.6 3.7 1920 1 US-08-746-789A-1 53.4 3.7 1905 4 US-09-055-113-2 48.4 3.3 7218 1 US-08-232-463-14 47.6 3.3 848 3 US-09-009-913-33 47.4 3.3 7218 1 US-08-232-463-14
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Sequence 3, Application US/08878177

Patent No. 6294354

GENERAL INFORMATION:
APPLICANT: Chugal Selyaku Kabushiki Kaisha, 5001, Iwamoto et ITILE OF INVENTION: Cell Calcification Suppressing Proteins of ITILE OF INVENTION: the Proteins Application Suppressing Proteins a FILE REFERENCE: chugal selyaku kabushiki kaisha 5001

CURRENT APPLICATION NUMBER: US/08/878,177

CURRENT FILING DATE: 1997-06-18

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 3

LENGTH: 1528

TYPE: DNA

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                                                          CGCCGAGCTATAACGCAGATATCCTCCTGTCACACCTACACTACCTCAGAGAGACTCCTC
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                                                                                                                                   Sequence 3, Application Patent No. 5968734 GENERAL INFORMATION:
           APPLICANT:
TITLE OF INV
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I: ZUCMAN, JESSICA
II. ZUCMAN, JESSICA
INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROU
INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
                                                               Melot, Thomas
Peter, Martine
Ploougastel, Beatrice
Thomas, Gilles
                                                                                                      Delattre, Olivier
Desmaze, Chantal
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STRANDEDNESS:
TOPOLOGY: line
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ACCACCAACGAGAGGAGAGTCATCGTCCCCGCAGACCCCCACACTGTGGACACAGGAGCAT
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                                                                                                                   CURRENT APPLICATION NUMBER: US/09/435,335
CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: 09/360,779
EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-03828
CURRENT FILIG DATE: 1999-07-26
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                           Sequence 1, application US/09435335 Patent No. 6384204 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                        APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the
TITLE OF INVENTION: Useful in the Treatment of Ne
FILE REFERENCE: CASE-04027
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                                                                 TYPE: DNA ORGANISM: Rattus
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NAME/KEY: CDS
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TYPE: DNA
ORGANISM: Rattus
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                                                                                                   LENGTH:
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Neurological D
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US-08-306-691B-43
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                             TELEFAX: (215) 568-554
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1119
                                                                                                            REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5849
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                             NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                      FILING DATE
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              STRANDEDNESS:
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                                             LENGTH:
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Two Penn Center, Suite 1800
                                             1604 base pairs
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linear
                                                                                                                                                                                                                                                                                                                                                                                                     Diskette, 3.50 inch, 720
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September 15, 1994
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Pred. No. 1.5e-51;
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                                    PCT-US93-06251-9
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Best Local Similarity
Matches 199; Conserv
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   Query Match
                                                                                                                                                TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 85; TELECOMMUNICATION INFORMATION: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona
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                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                   MOLECULE TYPE:
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TELEPHONE: 510-742-4366
                                                                   TOPOLOGY:
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                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                 LENGTH:
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                                                                                                                1604 base pairs
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 Score 124.6;
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; NAME/KEY: CDS
; LOCATION: (291)..(1700)
US-09-344-579-1
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US-09-344-579-1
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APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 2268
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION FILE REFERENCE: RTS-0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                             GCCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGCT 1134
                                                                                                                                           AAGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTCA 1074
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ACGTGTACCGCTTCGTGTGCGAC
                             ATGCCTACAAATTTGATTTCCAC 1157
                                                         GCCGGGGCTTACGCTACTATTACGACAAGAACATCATCCACAAGACGTCGGGGAAGCGCT
                                                                                                                         AGGTGGCCCGCCGGTGGGGAAAGAGGGAAAAATAAGCCCCAAGATGAACTACGAGAAGCTGA
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99; Conservative
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1625
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                   1134
                                                                                                                                                      1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENY INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and
STREET: Two Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 123..1769
OTHER INFORMATION: /D
OTHER INFORMATION: F3
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
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                                                                                                                                                                                                                                                                                                                                             Local
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TATGCCTACAAATTTGATTTCCACGGAATCGCTCAGGCCCTCCAGCC
                                                                                                                                                    GAAGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTC 1073
                                                                                  AGCCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGC 1133
                                                                                                                    GAGGTGGCCCGGCTGTGGGGCGTTCGCAAGTGCAAGCCCCAGATGAATTACGACAAGCTG
                                                                                                                                                                                     TACCAGGGCGTCATTGCCTGGCAGGGGGACTACGGGGAATTCGTCATCAAAGACCCTGAT
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                                                 AGCCGGGCCCTGCGCTATTACTATAACAAGCGCATTCTGCACAAGACCAAGGGGGAAACGG
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Factor) cDNA"
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Pred. No. 8.8
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                                         1074
                                                                                                               1014 GAAGTGGCTCGGCGTTGGGGAGAGAGGAAAAGCAAACCTAACATGAACTATGACAAACTC 1073
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    366
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                     AGCCGTGCACTTCGCTACTATGACAAAAATATTATGACTAAAGTTCATGGTAAACGC 1133
                                                                           GAGGTGGCCCGGCTGTGGGGCGTTCGCAAGTGCAAGCCCCAGATGAATTACGACAAGCTG 365
AGCCGGGCCCTGCGCTATTACTATAACAAGCGCATTCTGCACAAGACCAAGGGGAAACGG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE: 10-Feb-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 123..176
OTHER INFORMATION:
Factor) cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: SEQ ID NO: 1:
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63.1%;
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Pred. No. 8.8e-30;
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                                                                                                      US-08-343-443B-5
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US-08-343-443B-5
                                     Query Match
Best Local Similarity
Matches 178; Conserv
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                                                                                                                                                                                                                                  TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/1
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA;
APPLICATION NUMBER: FR 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: AEDIT 1.0 DOS text editor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                     FEATURE:
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733 CTTATGAGCAAGCGAGGAGATCAGCGTGGACGAGTCACAGCCATCC---CACTCAGTCAA 789
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                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 230 -- CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                   NAME: Weiser, Gerard
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/O FILING DATE: 18-NOV-1994
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                 328 base pairs
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230 South Fifteenth Street
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Ploougastel, Beatrice
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Desmaze, Chantal
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IBM PC compatible
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1..327
                                                                                                                                                                      linear
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                                                    8.0%;
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                                                                                                                                                                                                                                                                                                                    989.6121P
                                  Score 115.2; DB 2;
Pred. No. 1.2e-29;
0; Mismatches 83;
                                     Indels
                                                                  Length 328;
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US-08-875-944B-1
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US-08-875-944B-1
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                               Query Match
Best Local Sin
Matches 150;
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APPLICANT: FUJINAG
APPLICANT: YOSHIDA
APPLICANT: HIGASHI
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                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FU.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202), 628-5197
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: JP 07-020173
FILLING DATE: 08-FEB-1995
PRIOR APPLICATION NUMBER: PCT/JP96/000:
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUJINAGA, Kei
APPLICANT: YOSHIDA, KOİChi
APPLICANT: HIGASHINO, FUMİNİRO
TITLE OF INVENTION: CANCER CONTROL
NUMBER OF SEQUENCES: 5
                                                                                                                                           FEATURE:
                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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910 TACAGCTATGGCAGTTCCTACTGGAGCTTCTGTCGGACAGCTCCAACTCCAACTGCATCA 969
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                                                                                                                                                                                                                                                                                                                                 NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                                                                                                          TOPOLOGY:
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                                               Similarity
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                                                                                                                                                                                                                      2064 base pairs
                                                                                                                                                                                                                                                                       (202)
                                Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                          1..1386
                                                                                                                                                                          linear
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                                            62.5%;
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                                                                                                                                                                                                                                                                                                                     FUJINAGA-1
                               Score 96; DB
Pred. No. 1.8e
0; Mismatches
                                0;
                        DB 3; ...
. 1.8e-22;
. 90;
                                                          Length 2064
                               Indels
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US-09-116-049-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
FILE REFERENCE: UTSC:582
CURRENT APPLICATION NUMBER: US/09/116,049A
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VER. 2.0 .
SEQ ID NO 3
LENGTH: 2064
                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 5922688
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.5%; Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                1136 ACTATTATGAGAAAGGCATCATGCAGAAGGTGGCTGGAGCGTTACGTGTACAAGTTTG
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                           APPLICANT: Hung, Mien-Chie APPLICANT: Xing, Xiangming TITLE OF INVENTION: PEA3 is NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076
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                                                                           CITY: Houston
STATE: Texas
                                                                                                                  STREET:
                                        COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                              Application US/08780835B
                                                                                                                  E: ARNOLD, WH
P.O. Box 4433
Floppy disk
                                                                                                                                       WHITE AND DURKEE
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Pred. No. 1.8e-22;
0; Mismatches 90
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application Patent No. 6172212
GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/780,835B FILING DATE: 10-JAN-1997 CLASSIFICATION: 514
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/09/303,268
FILING DATE: 30-App-1999
CLASSIFICATION: CUnknown>
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UT
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ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                       APPLICANT: Hung, Mien-Chie Xing, Xiangming TITLE OF INVENTION: PEA3 is NUMBER OF SEQUENCES: 9
PRIOR
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Similarity 57.9%;
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ZIP: 77210-4433
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STATE: Texas
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APPLICATION
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FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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GCATCATGCAGAAGGTGGCTGGCGAACGCTACGTGTACAAGTTTGTGTGCGA 1606
                                       ATATTATGACTAAAGTTCATGGTAAACGCTATGCCTACAAATTTGATTTCCA 1156
                                                                                                                       GCAAACCTAACATGAACTATGACAAACTCAGCCGTGCACTTCGCTACTATGACAAAA 1104
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                                                                                 LENGTH: 2410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: UTSC500
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TELEFAX: (512) 474-7577
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   Query
                                 OZAWA R., NOGUCH1 H., Taylor T.D.,
"MUS muSculus Erg mRNA.";
Submitted (OCT-2001) to the EMBL/C
EMBL; AB073080; BAB69950.1; -.
MGD; MGI:95415; Erg.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR002341; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; ETS_DOMAIN.1; UI
PROSITE; PS00345; ETS_DOMAIN.2; UI
PROSITE; PS00346; ETS_DOMAIN.3; 1.
SEQUENCE 486 AA; 54614 MW; BET
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Eukaria; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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PS50061;
PS50105;
451 AA;
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ETS_DOMAIN_3; 1.
SAM_DOMAIN; 1.
; 51002 MW; 3E6C48BCA61
   92
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Pred. No. 2.5
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                                                       UNKNOWN_1.
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      Query
                                                         Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN.
PROSITE; PS00346; ETS_DOMAIN.
PROSITE; PS00346; ETS_DOMAIN.
PROSITE; PS00346; ETS_DOMAIN.
PROSITE; PS00346; ETS_DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                               plead for a role in endothelial cell differentiation.";
Dev. Dyn. 216:420-433(1999).
EMBL; AJ224126; CAB46567.1; -.
HSSP; O01543; IPLI.
InterPro: TBROACH
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Amphibia; Batrachia; A
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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01-DEC-2001
Erg protein.
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MEDLING=20099678; PubMed=10633861;

MEDLING=20099678, PubMed=10633861;

Mager-Heckel A.M.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT
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                                                            PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
PS50061; ETS_DOMAIN_3;
456 AA; 51482 MW; I
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      456;
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Best Loc Matches

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89.98;

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                                                                          Query Match
Best Local S
Matches 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-LIVER;
Aoki T., Toyoda H.,
"Identification of
                                                                                                                                                  InterPro; ITWAND | Pfam; PF00176; Ets; 1.
Pfam; PF00198; SAM_PNT; 1.
Pfam; PF02198; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; UNKNOWN_1.
PROSITE; PS00346; ETS_DOMAIN_2; UNKNOWN_1.
PROSITE; PS0061; ETS_DOMAIN_3; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91XV5 PRELIMINARY; PRT; 455 AA.
Q91XV5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Vascular endothelial cell specific protein 14.
                                                                                                                                                                                                                                                                                                               Submitted (AUG-1999) to the ELEMBL; AB031088; BAB62744.1; -
INTERFORM IPRO00418; ETS.
INTERFORM IPRO00341; HSF_ETS.
INTERFORM IPRO03118; SAM_PNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                   Similarity
                                                                             Conservative
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                                                                                                   89.2%;
                                                                          14;
                                                                          Score 2179; Di
Pred. No. 2.4e
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ρy
                                                                                                                                                                                                                                                               OZAWA R., NOGUCHI H., TAYLOR T.D., T.
"MUS MUSCULUS ETG MRNA.";
SUDMITTEG (OCT-2001) to the EMBL/Gen
EMBL; AB073079; BAB69949.1;
EMBC; MGI:95415; ETG.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR00318; SAM_PNT; 1.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalla; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                   PROSITE; PS00345; ETS_DOMAIN_1; UNKNOWN_1.
PROSITE; PS00346; ETS_DOMAIN_3; UNKNOWN_1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
SEQUENCE 463 AA; 51971 MW; 510D2BB7666
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                 ARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTN
                                                               LLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAPHPPALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTSHSHPT-QSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRP-----DLPYEQARRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTT
ARVTIKMECNPSQVNGSRNSPDECSVNKGGKMVGSPDTVGMSYGSYMEEKHVPPPNMTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTGHSHPTPQSKAAQPSPSTVPKTEDQRPQLDPYQILGPTSSRLANPGSGQIQLWQFLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASTIKEALSVVSKDQSLFECAYGTPHLAKTEMTASSSSDYGQTSKMSPRVPQQDWLSQP
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                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLIEL. 19,
(TrEMBLIEL. 19,
(TrEMBLIEL. 21,
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                 88.4%;
                                                                                                                                  12;
                                                                                                                                Score 2159.5;
Pred. No. 8.8e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                 510D2BB76663D4A4 CRC64;
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                                                                                                                                                                 DB 11;
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                                                                                                                                  163;
13;
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                                                                                                                                  Indels
                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sakaki Y.;
                                                                                                                                                                 463;
                                                                                                                                49;
                                                                                                                                Gaps
                                  121
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                                                                              Query Match
Best Local S
Matches 399
                                                                                                                             InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR0023118; SAM_PNT.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
PFNNTS; PR00454; ETSDOMAIN.
SMARR; SM00413; ETS; 1.
SMARR; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS00346; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                 Q9W700 PRELIMINARY;
Q9W700;
01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, L
01-DEC-2001 (TrEMBLrel. 19, L
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-20099678; PubMed-10633861;

Baltzinger M., Mager-Heckel A.M., Remy P.;

Baltzinger M., Mager-Heckel a.M., Remy P.;

"Xlerg: Expression and pattern and overexpression during plead for a role in endothelial cell differentiation.";

Dev. Dyn. 216:420-433(199).

Dev. Dyn. 216:420-433(199).
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Venamphibia; Batrachia; Anura; Mesobatrachia; Xenopodinae; Xenopus.
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                            HSSP; Q01543; 1FLI.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
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                  67
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                                                EALSVVSEDQSLFECAYGSPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQPPARVTI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTNERRVI
                                      EALSVVSEDQSLFECTYGTPHLTKTEMTASSSSDYGQTSKMSPRVPQQDWLSQPPSRVTI
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                                                                                        Similarity
                                                                                                                       485
                                                                               Conservative
                                                                                                                      AA;
                                                                                                                               ; ETS_DOMAIN_1;
; ETS_DOMAIN_2;
; ETS_DOMAIN_3;
                                                                                                                    54804 MW;
                                                                                       88.1%;
84.5%;
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Last annotation updat
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                                                                              Pred. No. 2.80
l; Mismatches
                                                                                                 Score
                                                                                                                      F87BF36DAFBA279F CRC64;
                                                                                      No. 2.8
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la; Pipoidea;
                                                                                        .8e-162;
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                                                                                                  DB 13;
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; Pipidae;
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                                                                             Gaps
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Best Local S
Matches 402
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01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Ozawa R., Noguchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                182
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                                                ERRVIVPADPTLMSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRLTP 181
                                                                                                                                                                                             SYNADILLSHLHYLRERGATFIFPNTSVYPEATQRITTRP----
                                                                                                                       ARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMTTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGQIQLWQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSR
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                                                                                                                                                                                                                                                                                       Similarity
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l (TrEMBLrel.
l (TrEMBLrel.
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                       88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor
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19,
21,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                      Score 2151; DB 11;
Pred. No. 4.1e-162;
6; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local
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InterPro; IPRO0341; HSF_ETS.
InterPro; IPRO03118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF00178; Ets; 1.
PFINTS; PR00454; ETSDOMAIN.
SMARF; SM00413; ETS; 1.
SMARF; SM00413; ETS; 1.
PROSITE; PS00346; ETS_DOMAIN.1; 1.
PROSITE; PS00346; ETS_DOMAIN.2; 1.
PROSITE; PS00346; ETS_DOMAIN.3; 1.
SEQUENCE 451 AA; 50655 MW; F4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PU61 PRE
Q9PU61;
01-MAY-2000 (Tr)
01-MAY-2000 (Tr)
01-DEC-2001 (Tr)
Fli-1 protein.
FLII OR FLI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mech. Dev. 90:237-252(2000).
EMBL; AJ249590; CAB56832.1; -.
HSSP; Q01543; IFLI.
ZFIN; ZDB-GENE-980526-426; fli1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20108585; PubMed-10640707;
Brown L.A., Rodaway A.R., Schilling T.F.,
Patient R.K., Sharrocks A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Insights into early vasculogenesis revealed by expression of the ETS-domain transcription factor Fli-1 in wild-type and mutant zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
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                                                                                                                                                                  LSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTK
                   TNERRVIVPADPTLWSTDHVRQWLEWAVKEYGLPDVDILLFQNIDGKELCKMTKDDFQRL 179
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PPARVTIKMECNPNQVNGSRNSPDDCSVAKGGKMVSSSDNVGMNYGSYMEEKHIPPPNMT
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                                                                                  -PVRVNVKREY--DHINGSRESPVDCSVGKCNKMVGGTEASQMNYTGYMDEKCAPPPNMT
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                    Score 1637; DB 15;
Pred. No. 2e-121;
""ematches 88;
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                                                                                          Query Match
Best Local S
Matches 304
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Pfam; PF00178; SAM_PNT; 1.
Pfam; PF002198; SAM_PNT; 1.
PRINTS; PR00454; ETS_DOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSTTE; PS00345; ETS_DOMAIN_1; 1
PROSTTE; PS00346; ETS_DOMAIN_2; 1
PROSTTE; PS00346; ETS_DOMAIN_3; 1
SEQUENCE 432 AA; 48761 MW; B3;
                                                                                                                                                                                                                                                                        Mager A.M., Grapin-Botton A., Ladjali K., Meye Stiegler P., Bonnin M.A., Remy P.;
"The avian fil gene is specifically expressed a subset of neural crest cells giving rise to Int. J. Dev. Biol. 42:561-572(1998).
EMBL; Y14773; CAA75078.1; -.
EMBL; Y14774; CAA75078.1; -.
EMBL; Y14774, CAA75078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLIEL 08, 01-NOV-1998 (TREMBLIEL 08, 01-JUN-2001 (TREMBLIEL 17,
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InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-98358003; PubMed-9694627;
                                                                                                                                                                                                                                                                                                                                                                                                                        Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                               Coturnix.
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                                           MASTIKEALSVVSEDQSLFECAYG-SPHLAKTEMTASSSSEYGQTSKMSPRVPQQDWLSQ 59
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APNPYWNSPTGGIYPNTRLPA---AHMPSHLGTYY
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                                                                                                    64.68;
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Last sequence up
Last annotation
                                                                                                   Score 1579.5; DB 13; Length 432; Pred. No. 6.7e-117;
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                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
                                                                                          .7e-117;
es 77;
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                                                                          InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR00233118; SAM_PNT.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PFAM; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PUL6;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                   PROSITE;
                                                                                                                                                                                    HSSP;
ZFIN;
                                                                                                                                                                                                                                                                                                       Dev.
                                                                                                                                                                                                           Thompson M.A., Ransom D.G., Pratt S.J., MacLennan H., Kieran Detrich H.W., Vail B., Huber T.L., Paw B., Brownlie A.J., Oat Fritz A., Gates M.A., Amores A., Bahary N., Talbot W.S., Her Beier D.R., Postlethwait J.H., Zon L.I.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=98294174; PubMed=9630750;

Thompson M.A., Ransom D.G., Pratt S.J., MacLennan H.

Detrich H.W.I.I.I., Vail B., Huber T.L., Paw B., Bro
Oates A.C., Fritz A., Gates M.A., Amores A., Bahary
Her H., Beier D.R., Postlethwait J.H., Zon L.I.;

"The cloche and spadetail genes differentially affec
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PUL6
                        NON_TER
                                        PROSITE;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            e cloche and spadetail genes differentially affect hematopoiesis vasculogenesis.";
                                                                                                                                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAASPYWTSPAGSIYPNPNVPRHPNAHVSPHLGSYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q01543; 1FLI.
ZDB-GENE-980526-426; fli1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAPNPYWNSPTGGIYPN---TRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTQSKATQPSSSTVPKTEDQRPQLDPYQIIGPTSSRLANPGSGQIQLWQFLLELLSDSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTSLYNTEVLLSHLSYLRESSSLLAY-NTPSHTEASSRLATKEGPPV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYKFDFHGIAQALQPHPTESSMYKYPSDLSYMPSYHAHQQKVNFVPPHPSSMPVTSSSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AGTQNVNKT---TEQQRPQPDPYQILGPTSSRLANPGSGQIQLWQFLLELLSDSSN
                                    PS00345; ETS_DOMAIN_1;
PS00346; ETS_DOMAIN_2;
PS50061; ETS_DOMAIN_3;
 414
414
                                                                                                                                                                                                                                                                                                                197:248-269(1998).
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(TremBLrel. 13, Last seq
(TremBLrel. 19, Last ann
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 46705
 MW;
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
 F68032D5F6C5C5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414
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Brownlie A.J.,
wary N., Talbot W.S.,
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                                                                                                                                                                                                                                                             A.C.,
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                                                                                               Query Match
Best Local S
Matches 218
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Best Local S
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                                                                                                                                           PRINTS: PRO0454; ETSDOMAIN.

SMART; SM00413; ETS; 1.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

SEQUENCE 476 AA; 51917 MW; AA7
                                                                                                                                                                                                                                                                                                                                                                                 Q9BZD1 PRELIMINARY; PRT; 476 AA.
Q9BZD1,
Q1BZD1,
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ewings sarcoma EWS-F111 (type 1) oncogene.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Ubhi T.B.S., Rainey D.R., Craig A.R., Meredith D.M.,

"The Ewings sarcoma EWS-Fli1 (type 1) oncogene.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databas

EMBL; AF327066; AAK11227.1; -.

HSSP; Q01543; IFLI.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                   InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS
Pfam; PF00178; Ets; 1.
   114
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                                                                                                          Local Similarity
                        52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQSAYGTQPAYPAYGQQPAATAPTRPQDG-
                      PQQDWLSQP--PARVTIKMECNPNQVNGSRNSPDDCS---VAKGGKMVSSSDNVGMNY-- 104
                                              QAQTTATYGQTAYATSYGQPPTGYTTPTAPQAYSQPVQGYGTGAYDTTTATVTTTQASYA 113
                                                                     EALSVVSEDQSLFECAYGSPHLAKTEMTASSS----SEYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYLRESSSSISY-NTPSHADQSPRLAAKDDASYDAVRTGWSNNMHSGKGSPTVVSQSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHINGSRESPVDCSVGKCNKMVGGTEASQMNYTGYMDEKCAPPPNMTTNERRVIVPADPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWSPDHVRQWLDWAIKEYGLQEIDTAMFHSTDGKELCKMSKDDFLRLTSVYNTEVLLSHL
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                                                                                               Conservative
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                                                                                                         39.5%;
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                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                             Score 965; DB 4;
Pred. No. 3.4e-68;
3; Mismatches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1486.5;
Pred. No. 1.5
                                                                                                                                             AA76AllE6CAE7A90 CRC64;
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-NKPTETSQPQSSTGGYNQPSLGYGQSNYSY
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                                                                                               130;
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                                                                                                                    Length 476;
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Best Local S
Matches 138
                                                                                                                                                                                                                                                Stapleton M., Brokstein P., Hong L., Agbayani A., (Champe M., Chavez C., Dorsett V., Farfan D., Frise Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Nunco J., Pacleb J., Paragas V., Park S., Phouanen Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datal EMBL; AY060316; AAL25355.1; Figh0000568; Ets65A.

InterPro; IPR000241; HSF_ETS.

Pfam; PP00178; Ets; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q95T62;
Q95T62;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                               PROSITE; PS00345; ETS_DOMAIN_1;
PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
SEQUENCE 257 AA; 28700 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dro
NCBI_TaxID=7227;
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                 343
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                                         84
                                                                                           27
YYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNF
                                                                                         SSYKSSWGSHS-STQSQGY--SSNALGIKHDPHSQLRQPDPYQMFGPTSSRLASSGSGQ
                                                                                                      QXVNEVPPHPSSMPVTSSSFFGAASQYWTSPTGGIYPNPNVPRHPNTHVPSHLGSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKMNEVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPN---TRLPAAHMPSHLGTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGSGQIQLWQFLLELLSDSANASCITWEGTNGEFKNTDPDEVARRWGQRKSKPNNNYDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTRPDLPYEQARRSAWTSHSHPTQSKATQPSSSTVPKTEDQRPQLDPYQILGPTSSRLAN
                                       IQLWQFTLELLSDSNNASCITWEGTNGEFKLTDPDEVARRWGERKSKPNMNYDKLSRALR
                                                     IQLMQFLLELLSDSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPTESSMYKYPSDISYMPSYHAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHP
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Eukaryota; Metazoa; Annelida; Polychaeta;
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PROSITE; PS00345; ETS_DOMAIN_1;
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PROSITE; PS50051; ETS_DOMAIN_3;
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EMBL; AJ311813; CAC44038.1; -.
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5; Mismatches 29;
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
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01-NOV-1996 (TrEMBLrel. 01, Cro
01-JAN-1999 (TrEMBLrel. 09, La:
01-DEC-2001 (TrEMBLrel. 19, La:
Hypothetical 41.5 kDa protein.
                                                                                                           "Direct Submission.";
Submitted (SEP-2001) to the
EMBL; U39470; AAC71120.1; -.
HSSP; Q01543; IFLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                       "The sequence of C. elec
Submitted (NOV-1995) to
                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
Stellyes L.;
                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a plinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q22355
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                       PRINTS;
                                                              InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                        Waterston
                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108н4.3
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Bocquet-Muchembled B., Leroux R.,
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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                    PF00178; Ets;
S; PR00454; ETS
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                                                                                                                                                                                                        R.;
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  ; ETSDOMAIN
ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
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Last annotation update
                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                       cosmid T08H4.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                           databases
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ng Consortium.";
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Best Local Sin
Matches 120;
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PROSITE; PS00346; ETS_DOMAIN_2;
PROSITE; PS50061; ETS_DOMAIN_3;
Hypothetical protein.
SEQUENCE 377 AA; 41466 MW; I
  286
                      355
                                                                                        166
                                                                                                                                    110
                                            226
                                                                  295
                                                                                                              258
                                                                                                                                               HNIPSFNMLSSYTGALKLSNSTSFANDDPYQILGPTSKNLAHSGSGQTQLWQFLLELLS
GKRYAYKFDFQGIAQALQ--PPTAS---HPQD--YFNS-HA----MGRIAP
           GKRYAYKFDFHGIAQALQPHPPESSMYKYPSDLPYMSSYHAHPQKMNFVAP
                                          DSSNSNCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVH
                                                                                                             QR-PQL------DPYQILGPTSSRLANPGSGQIQLWQFLLELLS
                                                                                                                                   DQSRRQFYTESSNSSGNGAAATSGSNGSSSSTESKSDVFNISMNAFAATPGS----KSED
                                                                                                                                                                                         Similarity
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                        41466 MW; D78A6BFA2472D409 CRC64;
                                                                                                                                                                                        21.4%;
                                                                                                                                                                             14;
                                                                                                                                                                                        Score 524; DB 5; Pred. No. 2.1e-33;
                                                                                                                                                                            Mismatches
                                                                                                                                                                               30;
                                                                                                                                                                                                  Length 377;
                                                                                                                                                                               Indels
  324
                      405
                                                                                                                                                                               67;
                                                                                                                                                                             Gaps
                                                                                                           294
                                            285
                                                                354
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Search completed: November 9, 2002, 16:53:25 Job time: 58.8288 secs